STIC-Biotech/ChemLib

From: Sent: To:

Kaushal, Sumesh Tuesday, May 03, 2005 5:45 PM STIC-Biotech/ChemLib 10657852: SEQ search

Subject:

10657852: SEO search Please search

SEQ ID NO:3

SEQ ID NO:15

S. Kaushal

AU1636, REM2.B85 Ph: 571-27-20769 Mail Box: REM2.C70

STAFF USE ONLY	
Searcher:	
Searcher Phone: 2-	Elala -
Date Searcher Picked	up:
Date Completed:	5/11/05
Searcher Prep/Rev. T	ime:
Online Time:	

Type	of Search
NA#:	AA#:
Interference:	SPDI:
S/L:	Oligomer:
Encode/Tran	sl:
Structure#:_	Text:
Inventor:	Litigation:

endors and cost where applicable	
STN:	
DIALOG:	
QUESTEL/ORBIT:	
LEXIS/NEXIS:	
SEQUENCE SYSTEM: QUILLED	
WWW/Internet:	
Other(Specify):	

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STIC Search Report Biotech-Chem Library

STIC Database Tracking Number

TO: Sumesh Kaushal Location: rem/2b85/2c70

Art Unit: 1636

Wednesday, May 11, 2005

Case Serial Number: 10/657852

From: Edward Hart

Location: Biotech-Chem Library

REM-1A55

Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Kaushal,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



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GenCore version 5.1.6
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OM protein - protein search, using sw model

May Run on:

9, 2005, 20:12:52 ; Search time 65 Seconds (without alignments) 2103.464 Million cell updates/sec

US-10-657-852A-15

Perfect score:

1385 1 MPEYMAKCCMLLVFLGFILQ......NTVSGSNHIVSGSNKVVTDG 267 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	O9m3w4 lolium pere	Q8h3w8 oryza sativ		Q63uhl burkholderi		Q9znx4 petunia hyb				Q940m7 arabidopsis	Q9fgq5 arabidopsis	Q69kc3 oryza sativ	Q84ng8 hordeum vul	Q66cj0 yersinia ps	Q75gm9 oryza sativ			Q9c9h7 arabidopsis	Q67tw5 oryza sativ		Q9srl7 arabidopsis	Q9zvr7 arabidopsis	Q8zgb5 yersinia pe		Q91964 moraxella c	Q6z0a9 oryza sativ	Q91s79 arabidopsis	Q8i4z3 plasmodium	Q91dg0 oryza sativ	Q9svnl arabidopsis	Q7xpi3 oryza sativ
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d	Query Match	38.3	18.9	18.7	16.0	15.7	15.3	14.7	14.5	14.4	14.3	14.3	14.2	14.1	14.0	14.0	14.0	14.0	13.9	13.9	13.9	13.8	13.8	13.7	13.7	13.6	13.6	13.5	13.5	13.4	13.4	13.4
	Score	530	262	258.5	221.5	218	212	204	201	199.5	197.5	197.5	196	195.5	194	194	194	193.5	192.5	192	192	190.5	190.5	190	189.5	188.5	188.5	187.5	186.5	186	186	185
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Oll-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative phytosulfokine receptor.
Name=P0885H11.109;
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzaa.
NCBI_TaxID=39947;

OCCOS GENTAL DAY DE CONTRACTOR DE CONTRACTOR

PRT; 1010 AA.

PRELIMINARY;

Q8H3W8 Q8H3W8;

RESULT 2 Q8H3W8

Q9sct4 arabidopsis Q6z15 oryza sativ Q6712 oryza sativ Q6712 oryza sativ Q9t54 moraxella c Q6et59 oryza sativ Q8115 oryza sativ Q61215 oryza sativ Q6121 oryza sativ Q6946 oryza sativ Q6946 oryza sativ	SI ,	W4 PRELIMINARY; PRT; 118 AA. W4; OCT-2000 (TrEMBLrel. 15, Created) OCT-2000 (TrEMBLrel. 15, Last sequence update) CCT-2000 (TrEMBLrel. 15, Last sequence update) CTV-2003 (TrEMBLrel. 24, Last annotation update) LTV-2003 (TrEMBLrel. 24, Last annotation update) LECTYStallisation inhibition protein (Fragment). Laryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Matophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; LaxID=4522;	York. EMBL/GenBank/DDBJ databases.	e recrystallisation inhibition protein. 0362ClE4F98AE9F8 CRC64; ore 530; DB 2; Length 118; ed. No. 3.5e-32; Mismatches 7; Indels 0; Gaps 0;	DEEPNTISGINNSVGSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVS 209 : : :	GTKHI VTDRNNVVSGNDNNVSGSFHTVSGEHNTVSGSRNTVSGSNHI VSGSNKVVTD 266
09SCT4 0623T9 0671T2 09XD54 09XD54 09LGT59 06R2J8 06R2J3 06R2J3 06SP46 08L7L6	ALIG	PRT; 5, Created) 5, Last see 4, Last and ibition pro ryegrass) 7, Streptophy yta; Liliop		ic Sc Fr	ANVVSGNDN :: ONVLAGNDN	WSGSFHTV WSGSFHTV
00000000000000		; 15, 15, 24, 115, 24, 24, 31, 15, 31, 15, 31, 31, 31, 31, 31, 31, 31, 31, 31, 31, 31, 31,	:y of the I	5 4 5 1 X	38GSP 18GSF	EN CASE
836 380 1051 1051 718 653 883 1065 7065 1080 983 983		PRELIMINARY; (TrEMBLrel. 1 (TrEMBLrel. 2 (TrEMBLrel. 1 Iliation inh ne (Perennial iridiplantae; a; Magnolioph; 522;	1.A. University 1.A. CAB87814. CAB87814. 1; A=1-118	L k	GTNNSV : : GSNNTVF	ININVVSC INININVSC
	·	PRELIN (Treme (Treme (Treme allisat nne (Pe /iridig (a, Mag	C.M.; 99), Unives ROM N.A. C.M.; (APR-2000) 7399; CAB8: Model; A=1	1 <1 .18 AA; .larity .Conser	PNTISC PNTISC	HIVTON
184.5 183.5 183.5 183.5 183.5 183.5 181.5 181.6 180.7	EL 40	Q9M3W4 Q9M3W4 Q9M3W4 Q9M3W4; Q1-OCT-2000 (TrEMBLrel. 15, C 01-OCT-2000 (TrEMBLrel. 15, L 01-UNN-2003 (TrEMBLrel. 24, L Lolium perenne (Perennial rye Bukaryota; Viridiplantee; Str Spermatophyta; Magnoliophyta; NCBL TaxID=4522;	JENCE Febottom sis (19 JENCE Febottom nitted i, AJ27	NON TER 11 CHAIN 11 SEQUENCE 118 AA; Query Match Best Local Similarity Matches 100; Conser	150 DEE : DEQ	210 GTK 61 GTN
W W W W W W W W W W W W W W W W W W W	SUL	97555555555555555555555555555555555555		FT NO FT CH SQ SE Query Best I	රු සු	& q

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RCLFLSLVALFALLPPPPAAAAPCHPEDLLALRAFAGNLSAGGGGGGGLRAAWSGDACCAW 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 -----GGISALLAAVSLRTANLSSNLLINDTLLDLAALPHLSAFNASNNSLSG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 LTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGT-----NNSVGSGSNNVVSG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 KCCML-LVFLGFILQVAGATSWSCHHDDLHALRGLAENLS-GKGAVRLRAAWSGASCCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned P1 clones."; DNS Res. 4:401-414(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR.2001 (TrEMBLrel. 16, Created)
01-MAR.2001 (TrEMBLrel. 16, Last sequence update)
05-Jul-2004 (TrEMBLrel. 27, Last annotation update)
Deutaive receptor protein kinase.
Name=At5g53890;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Exassicales; Brassicaceae; Arabidopsis.
                                                                                                                              R GO; GO:0004674; F:ATP binding; IEA.

R GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.

R GO; GO:0004672; F:receptor activity; IEA.

R GO; GO:0016740; F:traceptor activity; IEA.

R InterPro; IPR00160; Kinase_like.

R InterPro; IPR00160; IER_plant.

R InterPro; IPR00190; IER_plant.

R InterPro; IPR00190; IER_lixes.

R Fam; PR0019; Prot kinase.

R ProDom; PR00101; Prot kinase; 1.

R PROSITE; PR00101; PROTEIN KINASE DOM; 1.

R ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98162728; Pubmed=9501997;
Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.
                                                   clone:POS8SH11.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AP004342; BAC20742.1; --
                        Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1010;
                                                                                                                                                                                                                                                                                                                                                                                                                            18.9%; Score 262; DB 2; Length 10
40.1%; Pred. No. 5.5e-11;
tive 19; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    1010 AA; 109074 MW; 5CCB04E51E18AF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1036 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 40.1 nes 71; Conservative
                                                                                                          HSSP; P36897; 1IAS. Gramene; Q8H3W8; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
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SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 CE--TASGRUVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSL---QIRL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 KSLTTDSQSLGMGSI-NMLLHVSSRRTLDEEPNTISGTNNSVG-----SGSNNVVSG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68
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                                                                                                                                                                                                                                                                                                                                                               Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Pagugurcz From N.A.

Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Peng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
A Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
Bakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
Davis R.W., Ecker J.R., Theologis A., Southwick A., Shinozaki K.,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
C. Institutive Ballogis to the Ser/Thr protein kinase family.
EMBL; AR007441 BAB10719.1; -.
EMBL; AX091180; AAL136375.1; -.
EMBL; AX091180; AAL36375.1; -.
EMBL; AX091180; Piprotein serine/threonine kinase activity; IEA.
GO; GO:0004674; Fiprotein serine/threonine kinase activity; IEA.
GO; GO:0004674; Fiprotein activity; IEA.
Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninol P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Rawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Theologis M., Southwick A., Shinozaki K., Davis R.W., Ecker J.R. Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIRELEQLSLSGNY--LSGE---LSKNLSGLKSLLISENRFSDVIPD 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1036 AA; 114339 MW; 6DF9511FC2A4E261 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007090; LRR plant.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr pkin AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00019; LEURICHRPT.
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Pfam; PF00069; Pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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ID Q6
AC Q6
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Query Match
15.7%; Score 218; DB 2;
Best Local Similarity 30.9%; Pred. No. 1.1e-07;
Matches 55; Conservative 31; Mismatches 72;
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01-OCT-2000 (TrEMBLrel. 15, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGPS/D4 precursor (LRR protein S/D4)
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InterPro; IPR007090; LRR plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 VVTGSDNTVVGS-------NHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSG 238
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Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 ALRGLAENLSGKGAVRLRAAWSGASCCSWEGVGCETASGRVVALRLPKR-----GLGGI
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                                                                                                                                                                                                                                                            A Holden W. Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K., Benthal H., Thomson N.R., Bascon N., Beacham I.R., Brooks K., Brown N.R., Challis G.L., Cherevach I., Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D., Relthall T., Praser A., Hance Z., Hauser H., Holroyd S., Jagels K., Reith K.E., Maddlson M., Moule S., Price C., Quail M.M., Subbinowitsch B., Rutherford K., Sanders M., Simmonds M., Simmonds S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.; "Genomic plasticity of the causative agent of melloidosis, Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.; Burkholderia pseudomallei.", 101:14240-14245(2004).

B. Burkholderia Dasticity of the causative agent of melloidosis, Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).

R. EMBL; BX571965; CAH35630.1. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                          Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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Burkholderiaceae; Burkholderia.
NCBI TaxID=243160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99; Indels
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative outer membrane protein.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.0%; Score 221.5; DB 2 27.7%; Pred. No. 6.6e-08; tive 41; Mismatches 99
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                                                                                                     Burkholderia pseudomallei K96243
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                                                                                    ORFNames=BPSL1631;
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                                                                                                                                                                                                                            STRAIN=K96243;
PubMed=15377794;
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RESULT 5
0062KNS
10 062KNS
AC 062K
DT 25-0
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160 545 SGDSSTASGTNASATGENSTATGTDSTASGSNSTANGTNS--TASGDNSTASGTNASATG 602 161 -NSVGSGSNNVVSGND-----NTVVSGNNNHVSGSN-----NTVVTGSDNTVVGSNHV 207 603 ENSTATGIDSTASGSNSTANGINSTASGDNSTASGINASATGENSTATGIDSTASGSNST 662 208 VSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVT 265 MEDLINE=20317212; PubMed=10659200; DOI=10.1104/pp.123.2.699; Guyon V.N., Astwood J.D., Garner E.C., Dunker A.K., Taylor L.P.; Fischion and characterization of cDNAs expressed in the early stages of flavonol-induced pollen germination in petunia."; Physiol. 123:699-710(2000). Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids, lamiids, Solanales, Solanaceae, Petunia. Guyon V.N., Astwood J.D., Garner E.C., Dunker A.K., Taylor L.P.; Isolation and characterization of cDNAs expressed in the early stages of flavonol-induced pollen germination in petunia."; if the Sci. Adv. Plant Physiol. 123:699-710(2000). 106 SGNSLVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTN----Gaps Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N., Zhou L., Frager C.M.; 20; PubMed=15272880; DOI=10.1111/j.1365-313X.2004.02162.x; Guyon V., Tang W.H., Monti M.M., Raiola A., Lorenzo G.D., McCormick S., Taylor L.P.; "Antisense phenotypes reveal a role for SHY, a pollen-specific leucine-rich repeat protein, in pollen tube growth."; Plant J. 39:643-654 (2004). "Structural flexibility in the Burkholderia mallei genome."; Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004). EMBL; CP000010; AAJ48866.1; - . SEQUENCE 1012 AA; 94758 MW; S3C27D16C62FBBDE CRC64; Length 1012; TISSUE-Germinating petunia pollen treated with kaempferol; Guyon V., Astwood J.D., Taylor L.P.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A. TISSUE=Germinating petunia pollen treated with kaempferol; 72; Indels Last sequence update) Last annotation update)

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SWISS-PROT
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                               NNNHVSG------SINNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSG 224
                                                                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
campanulids, Apiales, Apiaceae, Apioideae, Scandiceae, Daucinae,
                                                                                                                                                                                                                                                            14 FLGFILQVAGAT---SWSCHHDDLHALR----GLAENLSGKGAVRLRAAWSGASCCSWEG
                                                                                                                                                                                                                                                                                                                     (By
                                                                                                                                                                                                                                                                                                     136 SINML--LHVSSRRTLDEEPNTISGTNN--SVGSGSNNVVSGNDNTVVSG-----
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                meristem, hypocotyl and root.

PTM: N-glycosylated

MISCELLANEOUS: A 36 amino-acid island is present in the 18th
leucine-rich repeat. An island domain has also been found among
the extra-cellular LRRs of the brassinosteroid receptor BRII and
has been shown to be critical for its finnetion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND GLYCOSYLATION. MEDLINE=22025707; PubMed=12029134; DOI=10.1126/science.1069607; Matsubayashi Y., Ogawa M., Morita A., Sakagami Y.; "An LRR receptor kinase involved in perception of a peptide plant hormone, phytosulfokine."; Science 296:1470-1472 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Phytosulfokine receptor precursor (EC 2.7.1.37) (Phytosulfokine LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Receptor with a serine/threonine-protein kinase activity. Regulates, in response to phytosulfokine binding, a signaling cascade involved in plant cell differentiation, organogenesis and sometic embryogenesis.

CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane
                                                                                          90; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
TISSUE SPECIFICITY: Expressed ubiquitously in leaf, apical
                                                                                                                                                                               VGCETASGRVVALRLPKR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              has been shown to be critical for its function. SIMILARITY: Belongs to the Ser/Thr protein kinase family. SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
                                                                Length 353;
               21 Potential.
38363 MW; 44CEA54EE2595COF CRC64;
                                                          15.3%; Score 212; DB 2;
ilarity 24.2%; Pred. No. 8.1e-08;
Conservative 50; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1021 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                          225 NDNNVSGSFHTVSG-----EHNTVSG 245
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353 AA;
                                                                       Local Similarity
nes 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor kinase).
Name=PSKR;
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                            SEQUENCE
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                                                            Query Match
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 Signal
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a collaboration
        between the Swiss Institute of Bioinformaties and the EMBL outstation—
the Buropean Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@lsb-sib.ch).
                                                                                                                  InterPro; IFROUSDI; MAK.
InterPro; IFROUSDI; MAK.
InterPro; IPRODO719; Pro_kinase.
InterPro; IPRODO719; Pro_kinase.
InterPro; IPRODO719; Pro_kinase.
If Proposed; LEWI, 16.
Promip Proposed; LEWICHRP, 1.
PROSITE; PRODO10; PROTEIN KINASE ATP; 1.
PROSITE; PSOOLO1; PROTEIN KINASE DOM; 1.
PROSITE; PSOOLO8; PROTEIN KINASE DOM; 1.
ATP-binding; Glycoprotein; Kinase; Leucine-rich repeat; Receptor;
Repeat; Serine/threonine-protein kinase; Signal; Transferase;
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(Potential)
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(Potential)
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It is produced through
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                                                                                                                                                                                                                                                                 Phytosulfokine
Potential.
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Protein kinase.
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N-linked
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N-linked
N-linked
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   entry is copyright.
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19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proton
                                                                                                  InterPro; IPR011009; Kinase like.
                                                                               EMBL; AB060167; BAC00995.1; -. HSSP; Q62838; 1LUF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112098
                                                                                                              IPR001611;
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1021 AA;
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183 EMMKNLVMLNASNNSFTGQIPSNFCSRSPSLTVLALCYNHLNGSIPPGFGNCLKLRVLKA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 GHNNLSGNLPGDLFNATSLEYLSFPNNELNGVINGTLIVNLRNLSTLDLEGNNINGRIPD 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 WSGASCCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 KSLQIRLKSLTTDSQSLGMGSINML---------LHVSSRRTLDEEPNT-- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 -----ISGTNINS-VGSGSNINVVSGNDN-TVVVSGNNNHVSGS-----NNTVVTG 196
                                                                                                                                                                                                                                                                                                                                                                                                                 12 KKCSNRCFIDFLRFNLAPALLILISLASPTS-SCTEQERSSLLQFLSSLGGLAV-SW 69
                                                                                                                                                                                                                                                                                                                                                                                 7 KCCMLLVFLGF-----ILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NHNNO----KHIVT----DNNNV-----
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                                                                                                                                                                                                                                                                                                                        98; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicacee, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 SIGQLKRLQDLHLGDNNISGELPSALSNCTHLITINLKRNNFSGNLSNVNFSN 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu
Maiti R., Ronining C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 -----VSGNDNNVSGSP----H--TVSGEHNTVSGSNNTVSGSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 784;
                                                                                                                                                                                                                                                               Length 1065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Town C.D., Kaul S.;
A Town C.D., Kaul S.;
L Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
L Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL, ACOIGIS, AAGS1813.1;
R InterPro; IPR001611; LRR.
DR InterPro; IPR001091; LRR. Dlant.
DR Pfam, PF00560; LRR 1; 20.
DR PRINTS; R000199; LEURICHEPT.
CONTROL OF TABLES CRC64;
                                                                                                                                                                                                             1065 AA; 116827 MW; CFE570663C05BF0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative disease resistance protein, 69620-67266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 14.4%; Score 199.5; DB 2; Best Local Similarity 24.2%; Pred. No. 1.9e-06; Matches 80; Conservative 51; Mismatches 80;
SMART; SM00169; LRR TYP; 8.
SMART; SM00210; S_TKG; 1.
SMART; SM0019; TYPIKG; 1.
PROSITE; PS50011; PROTEIN KINASE_ATP; UNKNOWN_1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                            Query Match
14.5%; Score 201; DB 2;
Best Local Similarity 24.6%; Pred. No. 2.1e-06;
Matches 87; Conservative 54; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 SDNTVVGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                               Kinase; Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
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                                                                                                                                                                                                          SEQUENCE
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                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                              119 HNSLSGSIAASLLNLSNLEVLDLSSNDFS---GLFPSLINLPSLRVLNVYENSFHGLIPA 175
                                                                                                                                                                                                                                                                                                59 FSSNCCDWVGISCKSSVSLGLDDVNESGRVVELELGRRKLSGKLSGESVAKLDQLKVLNLT 118
                                                                                                                                                                                                                                                                                                                                                                                 107 GNSLVGEVPKSL----QIRLKSLTTDSQSLGMGSINWLLHVSSRRTLDEEPNTISG---- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 -GASCCSWEGVGCETA-----SGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --TNN-----SVGSGSNNVVSGNDNTV--VSGNNNHVSG------SNNTVV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 TGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTV-----SGEHNTVS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 ALQNNRLSGA----LSSKLGKLSNLGRLDISSNKFSGKIPDVPLELNKLMYFSAQSNLFN 291
                                                                                                                                                                                  8 VILILVGFCVQIVVVNSQNLTCNSNDLKALEGFMRGLESSIDG------WKWNESSS 58
                                                                                                                                                    57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
He G.M., Li K.G., Yang J.S.;
"Oryza sativa (indica cultivar-group) chromosome 2 genomic sequence.";
submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                 10 MLLVFLGPILQ--VAGATSWSCHHDDLHAL----RGLAENLSGKGAVRLRAAWS----
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The G.M., Li K.G., Yang J.S.;

"Isolation and expression pattern of putative LRR (leucine-rich repeat) receptor-like kinase in rice.";

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AY730046; AA012611.; -..

EMBL; AY714494; AA012603.1; -..

R GO; GO:0004872; F:receptor activity; IEA.

R InterPro; IPR011009; Kinase_like.

R InterPro; IPR001095; Kinase_like.

R InterPro; IPR001095; LRR_Cyst.

R InterPro; IPR003591; LRR_Cyst.

R InterPro; IPR003591; LRR_Lyp.

R InterPro; IPR003591; LRR_Lyp.

R InterPro; IPR003591; LRR_Lyp.

R InterPro; IPR003290; Ser_thr_pkinase.

R InterPro; IPR001295; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last amotation update)
Putative leucine-rich repeat receptor-like kinase.
Oryza sativa (indica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                            98;
                                      Length 1021;
                                                                                         94; Indels
                                   14.7%; Score 204; DB 1; 24.6%; Pred. No. 1.2e-06; iive 56; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1065 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 GS------ 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 GEMPRSLSNSRSISLLSLRNNTLSGQIYL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00019; LEURICHRPT.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00365; LRR_SD22; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00560; LRR 1; 20.
Pfam; PF00069; Pkinase; 1
                                                                                            81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159
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                                                                                            Matches
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G-----HDNNVSGSFHTVSG-----EHNTVSGSNNTVSGSNH 255
    124 TELRFLDLSDNHISGALPASFGALSNLQVLNLSDNSFVGELPNTL-GWNRNL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  751 AA; 82062 MW; 180302F2B7EFF966 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.3%; Score 197.5; DB 2; 28.6%; Pred. No. 2.5e-06; ive 34; Mismatches 78;
                                                                                                                                                                                                                                                                                                      751 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Kinase Receptor:
SEQUENCE 751 AA; 82062 MW; 180302F2B
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007090; LRR plant.
InterPro; IPR000719; Prot_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67; Conservative
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001611; LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00560; LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eurosids II; Bra
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Tabata S.
                                                                                              175
                                                                                                                                        224
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                                                                                                                CSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSL--- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---QRDGLLKFRDEFPIFESKSSPWN 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Marusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                           91'PSSIGELDHLRYLDLSGNSLVGEVPKSL----QIRLKSLTTDSQSLG-----MGSINMLL
                                                                                                                                                                                                                                                                                                   226 BFRIFFNNFTSLPSD-----LSGFHNLVTFDISA----NSFSGHFPKFLFSIPSL
                                                                                                                                                                                                                                                                     HVSSRRTLDEEPNT1SGTNNSVGSGNNVVSGNDNTVVSGNNNHVSGS-----
                                                                                                                                                                                                                                                                                                                                                              -----NNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eddicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55,
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GO; GO:000524; F:RTP binding; IEA.
GO; GO:0004672; F:Protein kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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CMLLVFLGFIL-QVAGATSWSCHHDDLHALRGLAENLSGKGAVRLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD00001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
SEQUENCE 751 AA; 82086 MW; E6ADAB4370F49689 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     --VSGEHNTVSGSNNTVSGSNHIVSGSNKV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   751 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Mismatches
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                                                                                       58 GAS-CCSWEGVGCETASGRVVALRLPKR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 AWVSMDRNQFSG---PIEFAN--ISSSSKL
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Arabidopsis thaliana (Mouse-ear cress).
                                          CIITIYFSFLIHSLASPSLHFCRHD---
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InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007090; LRR plant.
InterPro; IPR000719; Prot_kinase.
Pfam; PF00560; LRR 1; 5.
PRINTS; PR0019; LEURICHRPT.
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les 67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 -QIRLKSLTTD-----SQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNVV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 SGNDNTVVSGNNNHVSG-----SNNTVVTGSDNTVVGS--NHVVSGTKHIVTDNNNVVS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secuence From M. A. Shinn P., Bowser L., Carninci P., Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Chen M. M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Nemann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narlusaka M., Southwick A., Tang C.J., Ouch H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., A. Toriumi M., Wallander E.K., Wong C., Wu H.C., Yamada K., Yu G., Yuan, S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

Smbli, BAD25614; BAB05647.1; --
RBBL, BT001094; AAN46893.1; --
RBBL, BT001094; Parre binding; IRA.

GO; GO:0004672; F:receptor activity; IRA.

GO; GO:0004672; F:receptor activity; IRA.

GO; GO:0006468; P:protein maino acid phosphorylation; IRA.
SGNDNTVVSGNNNHVSG----SNNTVVTGSDNTVVGS--NHVVSGTKHI VTDNNNVVS
                                                                         ----TEISLOKNYLSGGIPGGFKSTEYLDLSSNLIKGSLPSHFRGNRLRYFNASYNRIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 27, Last annotation update)
Receptor-like protein kinase (Arisg67280/K3617_4).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                   G-----HDNNVSGSFHTVSG-----EHNTVSGSNNTVSGSNH 255
                                                                                                                                                                                                    55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani
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58 GASCCSWEGVGCETA-SGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPK 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 SL----QIRLKSLTTDSQS----LGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 NVVSGNDNTVVSGNNNHVSG----SNNTVVTG---SDNTVVGSNHVVSGTKHIVTDNN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 TV-----AVPSVARNHVHGQVPPWLGNLTALEDLNWADN--IMSGHVPPALSKLINLRS 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hordeum vulgare (Barley).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural organization of the barley D-hordein locus in comparison with its orthologous regions of wheat genomes."; Genome 46:1084-1097(2003).
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REAL; AYZ68139; AAP31049.1.

REQ; GO:0005224; F:ATP binding; IEA.

RO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

RO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

RO; GO:0004872; F:receptor activity; IEA.

RO; GO:0016740; F:ransferase activity; IEA.

RO; GO:0016740; F:ransferase activity; IEA.

RO; GO:0016740; F:ransferase activity; IEA.

RO; GO:0006740; F:receptor activity; IEA.

RO; GO:0006709; K:ransferase activity; IEA.

RO; GO:0006709; K:ransferase activity; IEA.

RO; RO; RO; RO; RO; R. Plant.

R InterPro; IPR001611; IRR.

R InterPro; IPR00179; Prot kinase.

R InterPro; IPR008271; Ser kinase.

R Pfam; PR00560; IER 1: 17.
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                                                                                                                                                              307 IPESLGHIRTLEILTMSVNNLSGLVPPSLFNISSLTFLAMGNNSLV 352
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                                                                                                         233 FHTVSGEHNTVS----GSNN-----TVSGSNHIVSGSNKVV
                                                                                                                                                                                                                                                                                                                                                                                                                                01-000-2003 (TrEMBLrel. 24, Created)
01-00N-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
PubMed=14663527; DOI=10.1139/g03-071;
Gu Y.Q., Anderson O.D., Londeore C.F., Kong X.,
Lazo G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEAM; PF00560; LRR 1; 17.

PRINTS; PR00019; LEUR.CHRPT.

PRODOM; PD00001; PROFEIN KINASE ATP; UNKNOWN 1.

PROSITE; PS50010; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.
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Matches 84; Conservative
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Q84NG8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGNSLVGEVPKSL----QIRLKSLTTDS-----QSLG------------------------133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 VFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASC--CSWEGVGCE
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   230 GEIPSGFADEIPEDATVDLSFNQLTGQIPGFRVLDNQESNSFSG-NPGLCGSDH 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantee, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AP005966; BAD34184.1; -.
GO; GO:000524; F:ATP binding; IEA.
GO; GO:0004671; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Match 1102; Score 196; DB 2; Length 1102; Local Similarity 24.3%; Pred. No. 5.2e-06; les 84; Conservative 47; Mismatches 109; Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sagaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine/threonine-protein kinase; Transferase.
SEQUENCE 1102 AA; 119984 MW; B960CDE45175C68E CRC64;
                                                                                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein B1047H05.16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0019; LEURICHRPT.
Prodom; PD000001, Prot Kinase; 1.
SMART; SM00209; LRR TYP; 7.
SMART; SM00219; TKC; 1.
SMART; SM00219; TYC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR011009; Kinase_like.
InterPro; IPR001611; LRR.
InterPro; IPR001611; LRR.
InterPro; IPR001591; LRR. Jant.
InterPro; IPR002591; LRR. Lyp.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR001291; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PP00560; LRR_1; 24.
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                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00560; LRR 1; 2
Pfam; PF00069; Pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=B1047H05.16;
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                                                                                                                                    RESULT 12
069KC3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 LDLSGNSLVGEVPKSLQIRLKSLTTDSQSLGMG-----SINMLLHVSSRRT-L 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEEPNTISGINNSVGSGSNNVVSGNDNTVVS------GNNNHVSGSNNTVVTGSD 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : | | : | | : | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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"Insights into the genome evolution of Yersinia pestis through whole genome comparison with Yersinia pseudotuberculosis.";

Proc. Natl. Acad. Soi. U.S.A. 101:13826-13831(2004).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Hypothetical protein OSJNBa0018K15.10.
Name=OSJNBa0018K15.10;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yersinia pseudotuberculosis IP 32953.
Batceria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
NCBI_TaxID=273123;
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622 AA; 65230 MW; 30B8C7D77A3D73CD CRC64;
                                                                                                                                                                                                                                                                                             25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative exported protein precursor.
ORFNAmes=YPTB1413;
LTVA--INNLQGLIPPVLFNMSSLECLNFGSNQLSGS 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68; Conservative
                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                    RESULT 14
Q66CJ0
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075GM
075GM
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DT 07-JU
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234 TGLSSLGAGGNALAGELPGWIGEMAALETLDLSGNRFVGAIPDGISGCKNLVE----VD 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 KSLTTDSQSL------GMGSINM------LLHVSSRRTLDEEPNTISG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 TGSDNTVVGSNHV-----VSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNTVS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 TINISVGSG------SINIVVSGNDNTVVS------GNINHVSGSINITV--V 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 ---SVPGGFPRSSSLRVLDLSRNLLEGEIPADVGEAGLLKSLDVGHNLFTGELPESLRGL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                      Leu H.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWS--GASCCS
Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M., Chao Y.-Y., Hsing Y.-I.C., Chen G.-S., Chen H.-H., Liu S.-M., Chao Y.-T., Lee P.-F., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R., Chen Y.-L., Chang C.-H., Chung C.-I., Han S.-Y., Haides S.-H., Kau P.-I., Lee M.-C., Leu H.-I. Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Mu H.-P., Shaw J.-F.; Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Mu H.-P., Shaw J.-F.; Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Co., Go. 000461 to the EMBL/GenBank/DDBJ databases.

R. EmBL; AC144737; AATO1367.1, -
GO; GO: 0004674; F: Protein serine/chreonine kinase activity; IEA.
GO; GO: 0004674; F: Protein amino acid phosphorylation; IEA.
GO; GO: 0004648; P: Protein amino acid phosphorylation; IEA.
R. InterPro; IPR00159; Kinase-like.
R. InterPro; IPR00159; LRR Lyp.
R. InterPro; IPR00129; Ser Lhr pkinase.
R. InterPro; IPR001245; Tyr_pkinase.
R. Pfami Pf00660; LRR Lyp.
R. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRODOUG19, LETRICHRET.
PRODOM; PD0000019, LETRICHRET.
ProDom; PD0000019, LER TYP; 5.
SNART; SM00210; STKC; 1.
SNART; SM00210; TYRC; 1.
PROSITE; PS00117; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
ATP-binding; Hypothetical protein.
SEQUENCE 917 AA; 96507 MW; AE6DC9F7DD6E0B77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 26.3% Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 GSNNTVSG 252
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289 LSGNALTG 296
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9, 2005, 20:21:49

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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May 9, 2005, 20:18:45 ; Search time 16 Seconds (without alignments) 1605.617 Million cell updates/sec Run on:

US-10-657-852A-15 1385 1 MPEYMAKCCMLLVFLGFILQ......NTVSGSNHIVSGSNKVVTDG 267. Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
!: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
Result No.	Score	Query Match	* Query Match Length	DB	10	Description	
	190.5	13.8	1008	~	D84434	probable receptor	
7	190	13.7	622		AF0169	probable exported	
m	186	13.4	645		T05251		ы
4	184.5	13.3	836	~	T46070	hypothetical prote	a)
ı,	179.5	13.0			G84524	dise	<u>.</u>
9	176.5	12.	743		C84633	probable disease	u
7	173.5	12.5	590	7	B86440		ע
80	169	12.2	420	~	AE1857	hypothetical prote	a)
Ø.	168.5	12.5		~	G96746	cal	d)
10	168	12.1		~	C96519	probable disease r	u
11	164.5	11.9		N	H84421	probable receptor	
12	164	11.8		N	B85440	receptor kinase-li	.н
13	162.5	11.7		N	T05322	hypothetical prote	as
14	162	.11	773	~	T00502	probable receptor	
15	161.5	11.7		N	T00475	probable disease	u
16	161	11.6		•	T47727	hypothetical prote	as
17	161	11.6	907	•	A86460		_
18	159.5	11.5		~	T17462	disease resistance	a)
19	158.5	11.4	959	•	B84664	probable receptor-	
20	158	11.4	478	N	H86459	hypothetical prote	a
21	157.5	11.4	966	~	T10725	protein kinase Xa2	a
22	157	11.3		~	S61925	cyst wall protein	
23	156.5	11.3		~	A86383	76.4K protein kina	æs
24	156.5	11.3	928 1	~	D96558	probable protein k	¥
25	156	11.3	371	~	T49908	hypothetical prote	a)
26	156	11.5	638	~	T05606	protein kinase hom	E
27	155.5	11.	942	-	JQ1674	protein kinase TMK	~
28		11.	729	7	F86308	Similar to disease	a)
29	154.5	11.2	1143	~	T10636	hypothetical prote	a

hypothetical prote	probable disease r	probable receptor-	protein TiN15.9 [i	probable receptor	probable receptor-	probable disease r	probable protein k	hypothetical prote	receptor protein k	leucine-rich repea	probable receptor-	protein kinase Xa2	sericin MG-2 - gre	probable receptor	probable receptor-
T02361	T05257	B84852	G96524	A96557	H84632	T00971	F96557	F85343	T50851	T07079	B84782	T04313	C61615	E96631	B84659
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	153 11.			152.5 11,				151 10			150.5 10				

ALIGNMENTS

AF0169
probable exported protein YP01388 [imported] - Yersinia pestis (strain C092)
C;Species: Yersinia pestis
C;Species: Varsinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF0169

RESULT 2

R,Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. dano-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.M.; Davis, P.; Dougan, G.; Nature 413, 523-527, 2001 A,Title: Genome sequence of Yersinia pestis, the causative agent of plague. A,Rieference number: AB0001; MUD:21470413; PMID:11586360 A,Rieference number: AB0001; MUD:21470413; PMID:11586360 A,Status: preliminary A,Rolecule type: DNA A,Residues: 1-622 < KUR> A,Cross-references: UNIPROT:Q8ZGB5; GB:ALS90842; PIDN:CAC90217.1; PID:g15979437; GSPDB:CGGenetics: 1-622 < KUR> A,Genetics: 1-622 < KUR> A,Genetics: 1-622 < KUR> A,Genetics: PRO1388 A,Genetics: PRO1388 A,Genetics: A,Genetic	OY 144 SSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDN 176 1
43 NLSGKGAVRLRAAWSGASCCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRY 102	RESULT 4 T46070 hypothetical protein T18N14.120 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 16-Aug-2004 C;Accession: T46070 R;Delseny, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.; A;Accession: T46070 A;Accession: T6070 A;Accession: T6070 A;Accession: T6070 A;Accession: T836 - DEL- A;Accession: Gource: cultivar Columbia; BAC clone T18N14 C;Genetics: C;Genetics: A;Athap position: 3 A;Introns: 625/1 A;Note: T18N14.120 C;Superfamily: protein kinase homology
RESULT 3 T05251 probable disease resistance protein F18A5.210 - Arabidopsis thaliana C,Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: T05251 R;Bevan, M; Weber, N; Grueninger, D.; Schmidheini, T.; Bancroft, I.; Mewes, H.W.; Maye submitted to the Protein Sequence Database, February 1999 A;Reference number: Z15405 A;Accession: T05251 A;Molecule type: DNB A;Residues: 1-645 ABBA A;Molecule type: DNB A;Restidues: 1-645 ABBA A;Restimental source: cultivar Columbia; BAC clone F18A5 C;Genetics: A;Map position: 4 A;Introns: 216/1; 541/1 A;Note: F18A5.210 Query Match Best Local Similarity 22.1%; Pred. No. 3.8e-06; Matches 82; Conservative 46; Mismatches 115; Indels 128; Gaps 14;	Query Match 13.3%; Score 184.5; DB 2; Length 836; Best Local Similarity 25.7%; Pred. No. 6.7e-06; Matches 89; Gaps 15; Matches 82; Conservative 48; Mismatches 100; Indels 89; Gaps 15; OM 10 MLLVFLGFILLOVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSG 58 11;
OY 9 CMLLVFLGFILQVAGATSWSCHIDDLALRGLAENLSGKGAVRLRAAW-SGAS 60 :	.247NNTVSGSNHI 256 305 DSFSNLSSLVSLNLESNHL 323 SULT 5 \$254 bable disease resistance protein [imported] - Arabidopsis thaliana Species: Arabidopsis thaliana (mouse-ear cress) 2ate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

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87

Accession: G84524

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probable protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Daces 2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: B86440
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.C.A.; Li, J.H.; Li, Y.; Liu, X.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q9C867; GB:AE005172; NID:g11054670; PIDN:AAG27890.1; GSPDB:GN
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A.Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 QWRPEDPDFCNWNGVTCDAKTKRVITLNLTYHKIMGPLPPDIGKLDHLRLLMLHNNALYG 111
                                                                                                               GIIPSSIGELDHLRYLDLSGNSLVGEVPKS-----LQIRLKSLTTDSQSLGMGSIN 138
                                                                                                                                                                  71 GEIPPSLGTLSHLTFLDLSENKLVGQVPSSIGNLTKLMYLRLSINHLSGKS-SVSFANLT 129
                                                                                                                                                                                                                        139 MLLHVSSRRTLDEEPNTI---SGTNNSVGSGSNNVVSGNDNTVVS------GNNN 184
                                                                                                                                                                                                                                                                              130 KLIQLDIREN-DFEPELIPDMSRFHNLEGFGGGNFFGPFPTSLFTIPSLRWVNLRDSNNN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 BVPKSL-----QIRLKS-LTTDSQSLGMGSINMLLHVSSRRTLDEBPNTISG----- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 GQLKKLISNFNV---SNNFLVGQIPSDGVLSG-------FSKNSFIGNLNLCG- 207
                                  6 MKSCCSWLLLISLLCSLSNESQ------AISPDGEALLSFRNAVTRSDSFIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 -W--SGASCCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TIMSVGSGSINNVVSGN--DNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5. MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAA-----
                                                                                                                                                                                                                                                                                                                                                                   189 FTGHIDFGNSSLSSRLSYLSLADNNFDGPIPESISKFLNIVJLDLRNNSFSGPFPT 244
                                                                                                                                                                                                                                                                                                                                    ---HVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVV--SGNDNNVSGSFHT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein all0406 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 -KHV-----DVVCQDDSG-NPSSHSQSGQNQKKNSGKLLISAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 12.5%; Score 173.5; DB 2; Local Similarity 24.7%; Pred. No. 2.8e-05; nes 70; Conservative 44; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-590 <STO>
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Best Local S:
Matches 70
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        25
                                                                                                                 88
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C84633
C966193
C566196: Arabidopsis thaliana (mouse-ear cress)
C5, Species: Arabidopsis thaliana (mouse-ear cress)
C5, Species: Arabidopsis thaliana (mouse-ear cress)
C5, Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
C5, Date: 02-Jul-2004
C5, Date: 02-Jul-2004
C6, Date: 02-Jul-2004
C7, Mayam, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Jule 02-Jul-2004
Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
Affitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:Q9ZUX3; GB:AE002093; NID:g4115363; PIDN:AAD03365.1; GSPDB:GN
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 TNHFVGKIPSSL------GNLSHL----TSIDLHKNNFVGEIPFSLGNLSCLTSF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----KRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 NDFIGQIPSSLETLSNLTTLDLSRNHFSGRIPSSIGNLSHLIFVDFSHNNFSGQIPSSLG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 IRLKSLTTDSQSL------GMGSINML--LHVSSRRTLDEEPNTISG------ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y-LSHLTSFNLSYNNFSGRVPSSIGNLSYLTTLRLSRNSFFGELPSSLGSLFHLTDLILD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TKH 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 ILSDNNIVGEIPSSFGNLNQLDILNVKSNKLSGSFPIALLNLRKLSTLSLFNNRLTGTLP 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 MKGYITLSFLILLIFNFLDEFAASTRHLCDPDQSDAILEFKNEFETLEESCFDSNIPLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TINNSVGSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSG-
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                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 179.5; DB 2;
; Pred. No. 1.9e-05;
56; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 AAWSGAS-CCSWEGVGCETASGRVVAL-------
                                                                                                                                                                                                                                                                                                                                                                                                                    13.0%; 21.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81; Conservative
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Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-983 <STO>
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-743 <STO>
                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                    A,Gene: At2g15080
A,Map position: 2
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A,Gene: At2g24160
A,Map position: 2
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13

Gaps

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probable disease resistance protein, 3954-7013 [imported] - Arabidopsis thaliana Cippedies: Arabidopsis thaliana (mouse-ear cress)
Cjoate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Ander, C.W.; Chung, M.K.; Comn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q9C699; GB:AE005173; NID:g10092530; PIDN:AAG12927.1; GSPDB:G
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     ---VLDLSYNSFKGELPLQQSFGNGSNGIFPIQTVDLSSNLLEGEILSSS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 NDNTVVSGNNMHV----SGS-----NNTVVTGSDNTVVG---SNHVVSG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 YLDLSGNSLVGEVPKSLQIRLKSLTTDSQS--
                                                                                                     192 VFLQGAFNLTSFNVSNNSFTGS
                                                               183 NNHVSGSNNTVVTGSDNTVVGS
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Best Local Similarity
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A;Residues: 1-1019 <STO>
        SALDQLL-
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Accession: G96746
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.;
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.S.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: G95746
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1095 <STO>
A; Coss-references: UNIPROT: Q9C7S5; GB: ABE005173; NID: g10645385; PIDN: AAG21504.1; GSPDB: G. Chooner manner.
                                                 ',Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
                                                                                                     DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                       Cross-references: UNIPROT:Q8YZQ1; GB:BA000019; PIDN:BAB72364.1; PID:g17129751; GSPDB:d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---DNTVV-----SGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 RVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLKSLTTDSQSLGM 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 FILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAW-SGASCCSWEGVGCE-TASG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FFLTVSEAV---CNLODRDSLLWFSGNVSSPVS---PLHWNSSIDCCSWEGISCDKSPEN 92
Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
Accession: AE1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 TDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNN-SVGS-----GSNNVVSGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /4e-05;
ches 51; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ••
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                                                                                                                                                                                                                                                                                                                                                                                                                                               12.2%; Score 169; DB 2; Length 420; 31.5%; Pred. No. 4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNDNNVSGSFHTVSGEHNTVSGSNNTVSGS-NHIVSGSNKVVTDG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | | : : | | | | | : | | | : | | 384 | GNGNWYFGTDNTTIGNGNWDFGTNNTILGNGNWIFTNNTVVGNG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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Pred. No. 0.00014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.2%; Sco., 12.0. ... 28.7%; Pred. No. v... 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                             A;Residues: 1-420 <KUR>
A;Cross-references: UNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                      Status: preliminary; Molecule type: DNA
                                                                                                                                                                                               A; Accession: AE1857
A; Status: prelimina:
A; Molecule type: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: T9N14.20
                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: all0406
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S:
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224
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                                                                                                                                                                                                                                                                                                                                                              Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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A,Accession: T00502
A,Status: translated from GB/EMBL/DDBJ
A,Reclecule type: DNA
A,Residues: 1-773 <ROU>
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       셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor kinase-like protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Reb-2001 #sequence_revision 16-Peb-2001 #text_change 16-Aug-2004
C;Accession: B85440
R;anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Sprint Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUD:20083488; PMID:10617198
A;Accession: B85440
A;Accession: B85440
A;Accession: preliminary
A;Accession: preliminary
A;Redeule type: DNA
A;Residues: 1-766 <STO>
A;Across-references: UNIPROT:023161; GB:NC_001268; NID:g7270708; PIDN:CAB80391.1; GSPDB:G
       ij
                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9ZU46; GB:AE002093; NID:g4262228; PIDN:AAD14521.1; GSPDB:GN
Genetics:
A;Gene: At2g01210
A;Map position: 2
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, I euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-716 <STO.>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----KSL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 SPCSWRGISCNNDS-KVLTLSLPNSQLLGSIPSDLGSLLTLQSLDLSNNSFNGPLPVSFP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 QI------RLKSLTT--DSQSLGMGSINM-LLHVSSRRTLDEEPNTISGT-- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : |||| ||: || || : :|:::|
158 SLRNLTVVSLENNYFSGE-----IPGGWRVV----EFLDLSSNLINGSLPPDFG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 ---QIRLKSLTTDSQS----LGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNVV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 SGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSG----- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                60 SCCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSL-
                                                                                                                                                                                                                                                                                                                                                                                                                    10 MLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAW--SGASCCSWEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 DGFGSAFVSLEKLDLAFNQFNGSIPSDIGNL--SNLQGTADFSHNHFTGS 225
                                                                                                                                                                                                                                                                                                                                                                           55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                                                                                              DB 2; Length 716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------NNSVGSGSNNVVSGNDNTVVSGNNNHVSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 11.8%; Score 164; DB 2; Length 766; 1 Similarity 28.5%; Pred. No. 0.0002; 63; Conservative 35; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 GCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVP-
                                                                                                                                                                                                                                                                                                                                                                         78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----HNTVSGSNNTVSG 252
                                                                                                                                                                                                                                                                                                                         11.9%; Score 164.5; DB 2 27.4%; Pred. No. 0.00017; ive 34; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 -- NDNNVSGSFHTVSGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::
                                                                                                                                                                                                                                                                                                                                                                         63; Conservative
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 63; Conserv
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Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Genetica:
A,Gene: AT4g37250
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A,Incrons: 863/1; 1116/1
A,Note: F1C12.60; F18F4.240
C,Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology; pı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I.; Mewes, H.W.; Mayer, K.F.X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.C.; Sykes, S.M.; Kaul,
                                                                                                                                                                                             NiAlternate names: hypothetical protein FIC12.60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05322; T04888
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15408
A;Accession: T05322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable receptor-like protein kinase At2g23300 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 EGVGCE-TASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NNHVSG------SNNTVVTGSD 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NyAlternate names: protein kinase homolog T20D16.7
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Aug-2004
C;Accession: T00502; A84623
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, November 1997
A;Bescription: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : | | | | : | : | | : | | | 4 LVLLLLFILCFSGLGQPGIINNDLQTLLEVKKSLVTNPQEDDPLR---QWNSDNINYCSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 SLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNN--SVGSGSNNVVSGNDNTVVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LLVFLGFILQVAGATSWSCHHDDLHAL----RGLAENLSGKGAVRLRAAWS--GASCCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
203 GYSLQYLNVSFNQISGEIPPEIGVNFPRNVTVDLSFNNLTG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Residues: 1-1232 - SBEV-
A,FCROSS-references: UNIPROT:QSSN91; EMBL:AL022224
A,Experimental source: cultivar Columbia; BAC clone F1C12
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft,
submitted to the Protein Sequence Database, February 1998
A,Reference number: 215388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 NTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 NMLNGTIPAELGR----LENLEILNLANNSLTGEIPSQLGE 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: cultivar Columbia; BAC clone F18F4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.7%; Score 162.5; DB 2; Best Local Similarity 25.3%; Pred. No. 0.00045; Matches 71; Conservative 41; Mismatches 94;
                                                                                                                                                                       hypothetical protein F18F4.240 - Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: AL021637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 N-----
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A; Residues: 1-305 < BEW>
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16;

Gaps

; Score 161.5; DB 2; Length 905; ; Pred. No. 0.00037; 45; Mismatches 105; Indels 143;

68

158

--LHVSSRRTLDEEPNTISG----

-----TVVSGNNN-----HVSGSNNTV 193

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69 VLCDARTSHVVKIDLRNPSQDVRSDEYKRGSLRGKIHPSLTQLKFLSYLDLSSNDFNELE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 LSSLSSSLKYLNMGYVNLSGAGETWLQDFSRISALKELHLFNSE-LKNLPPTLSSSADLK 247
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                                                                                                                                                                                                                                                                                                                                                                  67 VGCETASGRVVA--LRLP-----KRG--LGGI-----
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                                                                                                            11.7%;
23.1%;
                                                                                                        Query Match 11.7%
Best Local Similarity 23.1%
Matches 88; Conservative
          A;Gene: F1913.16; At2g34930
A;Map position: 2
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Job time : 18 secs
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A;Cross-references: UNIPROT:022178; EMBL:AC002391; NID:g2642427; PID:g2642433
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rouneley, S.D.; Bhito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Alature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 LGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSL----QIRLKSLTTDSQS----LGMGSI 137
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195 VQYLDISSNLINGSLPPDFSGDNLRYLNVSYNQISGEIPPNVGAGFPQNATVDFSFNNLT 254
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                                                                                                                                                                                                                                                                                                                                                        Residues: 1-773 <STO>
Cross references: GB:AE002093; NID:g2642433; PIDN:AAB87101.1; GSPDB:GN00139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.7%; Score 162; DB 2; Best Local Similarity 27.3%; Pred. No. 0.00028; Matches 66; Conservative 36; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: At2g23300; T20D16.7
A,Map position: 2
A,Introns: 545/1
C,Superfamily: protein kinase homology
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                                                                                                                                                                                                                                                          A;Accession: A84623
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-773 <STC
A;Cross-references: G;Genetics:
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Sequence 9, Appli
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Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 902, Appl
Sequence 90, Appl
Sequence 17, Appli
Sequence 7, Appli
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Sequence 934, Appl
Sequence 936, Appl
Sequence 2676, Appl
Sequence 936, Appl
Sequence 937, Appl
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1 MPEYWAKCCMLLVFLGFILQ.....NTVSGSNHIVSGSNKVVTDG 267
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/ReCOMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-952-267B-9

US-09-952-267B-5

US-09-36-247A-15

US-09-352-267B-15

US-09-352-267B-15

US-09-36-247A-15

US-10-101-464A-893

US-10-101-464A-902

US-09-22B-986-80

US-10-101-464A-902

US-09-352-267B-7

US-09-352-267B-7

US-10-101-464A-934

US-10-101-464A-944

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Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence 16, Appl Sequence 13, Appl Sequence 13, Appl Sequence 3401, Appl Sequence 79, Appl Sequence 72, Appl Sequence 72, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 75, Appl Sequence 76, Appl Sequence 77, Appl Sequence 70,	OF MORAXELLA CATARRHALIS	Length 941; 10; Indels 6; Gaps 1; INTUVICSDNITUVGSNHTUVSGTKH 213
4 US-09-345-473E-16 3 US-09-336-447A-13 4 US-09-52-267B-13 4 US-09-540-236-3401 4 US-09-240-36-3401 5 US-09-228-986-79 6 US-10-101-464A-72 6 US-10-101-464A-72 7 US-09-336-447A-1 7 US-09-36-47A-1 6 US-10-101-464A-944 7 US-09-228-986-75 6 US-09-228-986-75 6 US-09-228-986-75 7 US-09-228-986-75 6 US-10-101-464A-75 7 US-09-228-986-75 8 US-09-228-986-75 8 US-09-228-986-75 8 US-09-228-986-75 8 US-09-228-986-75 8 US-09-228-986-75	ALIGNMENTS 6447A C19/336,447A 21	182; DB 3; No. 1e-08; matches 50; SGNNNHVSGSNNT
10.8 645 10.8 873 10.8 873 10.8 873 10.6 711 10.6 910 10.6 635 10.5 10.5 831 10.5 10.5 160 10.4 659 10.3 655	ion US/0 ERIC J. HRISTOPH ESLIE D. TISBED D. MICHAEL URG, ROS USPA1 A NUMBER: 1999- S: 98 S: 98 Ver. 2.1	tch al Similarity al 21s; Score 182; al Similarity 34.2s; Pred. No. 1 39; Conservative 19; Mismatch 11st NTISGTNNSVGSGSNNVVSGNDNTVSGNNN 11st NTISGTNNSVGGANNQAKGNYSTVGGKGNNN 11st NEAMERSTVAGGANNQAKGNYSTVGGKGNN 11st IVTDNNNVSGNDNNVSGSFHTVSGEHNTVS 11st IVTDNNNVSGSFHTVSGEHNTVS 11st
28 1499 30 1499 31 1499 33 1499 34 1490 36 1490 37 1490 38 1490 39 1490 40 1400 40 1400 40 1400 40 1400 40 1400 40 1400 40 1400 40 1400 40 1400 40 1400 40 1400 40 1400 40 1400 40 1400 40 1400 40 1400 40 40 40 40 40 40 40 40 40	RESULT 1 US-09-336-447A-9 Sequence 9, Applicat Patent No. 6310190 GENERAL INFORMATION: APPLICANT: ABBI, C. APPLICANT: COPE, L. APPLICANT: COPE, L. APPLICANT: PREDENB, APPLICANT: PREDENB, APPLICANT: PREDENB, APPLICANT: PRESENG,	Query Match Best Local Similarit Matches 39; Conse Qy 154 NTISGTWN Cy 214 IVIDNNNV Qy 214 IVIDNNNV Cy 214 IVIDNNV Cy 214 IVIDNNV CY 214 IVIDNNV CY 214 IVIDN CY CY 214 IV

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TYPE: PRT
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APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDEMBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HANSEN, ERIC J.
APPLICANT: ABBL, CRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: WEBDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
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CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SSOFWARE: Patentin Ver. 2.1
SSOFIND S
LENGTH: 892
PRIOR APPLICATION NUMBER: US/09/336,447
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
FENOM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09336447A
Patent No. 6310190
GENERAL INFORMATION:
APPLICANT: HANNEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: OOPE, LEGLIE D.
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                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-952-267B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 31.8<sup>1</sup>
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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US-09-336-447A-5
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                                                                                                                                                  LENGTH: 941
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Sequence 890, Application US/10101464A
Patent No. 6768041
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
APPLICANT: Higgins, Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.102002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 DPYGWLSNWTANNSHNVCLWNGISCSPNTNRVVEISLRYGRLNGTLSPYIGNLSLRHLD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104
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                                                                                                                                                                                                                                                                                                   Length 892;
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; Pred. No. 2.8e-08;
54; Mismatches 105;
                                                                                                                                                                                                                                                                                                   Query Match 12.8%; Score 177; DB 4; Best Local Similarity 31.8%; Pred. No. 2.9e-08; Matches 35; Conservative 20; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURKENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR PELING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR PELING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR PELING DATE: 1999-11-01
PRIOR PELING DATE: 1999-11-01
PRIOR PELING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FASESEQ for Windows Version 4.0
FEDUTOR OF SEQ ID NOS: 989
CURRENT APPLICATION NUMBER: US/09/952,267B
CURRENT FILING DATE: 2001.09-12
PRIOR APPLICATION NUMBER: US/09/336,447
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/101,464A CURRENT FILING DATE: 2002-03-18
                                                                                                                                                                                                     TYPE: PRT ORGANISM: Moraxella catarrhalis
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Best Local Similarity 25...
Best Local 77; Conservative
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Best Local Similarity
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                                                                                                                                                                           LENGTH: 892
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US-09-952-267B-15
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                    ---VSGND 226
                                               239 NCTSLTDLVISSNNLSGPIPSEFSGLVSLKFLFLDDNSISGSIPTSLVNCTSLFALKGSG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 TTDSQSLGMGSINMLLHVSS------RTTLDEEPNTIS-GTNNSVGSGSNNVV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 SGNDNITVVSGNNNHVSGSNNITVVIGSDNITVVGSNHVVSGTK--HIVIDNNNVVSGNDNNV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: FISKE, MICHEL J.
APPLICANT: PREDRING'S, ANCY:024
CURRENT APPLICATION NUMBER: US/09/952,267B
CURRENT PILING DATE: 2001-09-12
PRIOR PLING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 999-06-21
NUMBER OF SEQ ID NOS: 999-06-21
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                                                                                                                                                                                                                                                                                                                     APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: MACIVER, ISOBEL
APPLICANT: FREDENBUG, ROSS A.
TITLE OF INVENTION: USPAI AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERRACE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.6%; Score 175; DB 3; Length 889; Best Local Similarity 27.1%; Pred. No. 4.5e-08; Matches 48; Conservative 25; Mismatches 66; Indels 38;
                    --IGSDNTVVGSNHV-----VSGTKHIVTDNNNV
                                                                                                                                 299 NKLSGPIPSVMGLMKSISTIDLSNNSLTG 327
                                                                                                      227 NNVSGSFHTVSG---EHNTVSGSNNTVSG 252
                                                                                                                                                                                                                                                        Sequence 15, Application US/09336447A Patent No. 6310190 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09952267B Patent No. 6753417 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Moraxella catarrhalis
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ORGANISM: Moraxella catarrhalis
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US-09-336-447A-15
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LENGTH: 889
                    195
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                                                                                                                                                                                                                                                                                                                                                                                                                      63 SWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRL 122
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22.7%; Pred. No. 5.2e-08;
tive 55; Mismatches 107; Indels 110; Gaps
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                                                                                         38;
Length 889;
                                                                                         25; Mismatches 66; Indels
12.6%; Score 175; DB 4; 27.1%; Pred. No. 4.5e-08;
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CCATION: (1)...(843)
COTHER INFORMATION: Xaa = Any Amino Acid
US-10-101-464A-893
                                                                                                                                                                                   126 TTDSQSLGMGSINMLLHVSS----
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Best Local Similarity 22.7%
Matches 80; Conservative
Query Match
Best Local Similarity 27.1%
Matches 48; Conservative
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ORGANISM: Pinus radiata
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## APPLICANT: Higgins, Colleen M.

### TITLE OF INVENTION: Compositions Isolated from Plant Cells

### TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

### TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

### TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

### TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

### CURRENT APPLICATION NUMBER: 09/104,302

### PRIOR FILING DATE: 2000-01-12

### PRIOR FILING DATE: 1999-01-01

### PRIOR FILING DATE: 1999-01-01

### PRIOR FILING DATE: 2000-01-11

### PRIOR FILING DATE: 2000-01-11

### RIOR FILING DATE: 2000-01-11
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Patent No. 6359198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Mieuwenhuizen, Miels
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
FIRE SERIES FARENCE: TENNER DATE: 100 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 RLRGTLSDSLGRLAHLREINVSFNLLTGEVPGRLFL-LQHL--EVLDLSFNNLSVIAPVA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 GLGGIIPSSIGELDHLRYLDLSGNSLVGEVPXSLQIRLKSLTTDSQSLGMGSINMLLHV- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 QSWKGVSCSGSS--VTLIKLSGLGLSGSLYYQLSSDLSSLTTLDLSNNNIQGNIPYALPQK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 -SWEGVGCETASGRVVALRLPKRGLGGIIPSSIGBLDHLRYLDLSGNSLVGEVPKSLQIR 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 CHHDDLHALRGLAENLSGKGAVRLRAAWS-GASCCSWEGVGCETASGR----VVALRLPKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 CMLLVFLGFILQVA---GATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWS--GASCC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.3%; Score 170.5; DB 4; Length 386; 32.3%; Pred. No. 3.8e-08; ive 25; Mismatches 61; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 707;
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Best Local Similarity 26.1%; Pred. nc.
Warrhes 81; Conservative 39; Mismatches
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Best Local Similarity 32.3%
Matches 52; Conservative
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ORGANISM: Pinus radiata
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ORGANISM: Pinus radiata
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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Micuwenhulzen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.10202
CURRENT APPLICATION NUMBER: 09/704,302
PRIOR PLILING DATE: 2000-11-01
PRIOR PELICATION NUMBER: 60/162,866
PRIOR PELICATION NUMBER: 60/162,866
PRIOR PELICATION NUMBER: PCT/US00/00724
PRIOR PUMBER: PCT/US00/00724
PRIOR PUMBER: PCT/US00/00724
PRIOR PUMBER: PCT/US00/00724
PRIOR PUMBER: PCT/US00/00724
253 SRLVRLETLLFDDNSISGSIPASISNCTSLQYLDISDNSLSGP------IPSEFSRL 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 --TGSDNTVVGSNHVVSGTKHIVTDNNNVVS-----GNDNNVSGSFHTVSGEHNT---VS 244
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25.5%; Pred. No. 2.4e-08;
tive 52; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 764, Application US/10101464A Patent No. 6768041 GENERAL INFORMATION:
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Patent No. 6766041
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 GSNNTVSGSNHIVSGSNKVVT 265
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Best Local Similarity 25.5
Matches 82; Conservative
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; ORGANISM: Pinus radiata
US-10-101-464A-764
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US-10-101-464A-902
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154 NTISGTNNSVGSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKH 213
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APPLICANT: MACIVER, ISOBEL
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBUG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REPERBUGS: AMCY:024
CURRENT APPLICATION UNMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
12.3%; Score 170; DB 3; Length 624;
Best Local Similarity 30.6%; Pred. No. 8.3e-08;
Matches 38; Conservative 24; Mismatches 50; Indels
                                                                      Sequence 7, Application US/09336447A
Patent No. 6310190
GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Moraxella catarrhalis
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SEQ ID NO 7
LENGTH: 624
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US-09-952-267B-7
RESULT 13
US-09-336-447A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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; Sequence 80, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Strabala, Timothy
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT APPLICATION NUMBER: 09/704,302
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR PILING DATE: 1999-01-10
; PRIOR PILING DATE: 1999-01-10
; PRIOR PILING DATE: 1999-01-10
; PRIOR PILING DATE: 2000-01-11
; PRIOR PILING DATE: 2000-01-11
; RIOR RELING DATE: 2000-01-11
; RIOR RELING DATE: SOURCE SEQ ID NOS: 989
; SOUTHWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                     61 QSWKGVSCSGSS--VTLIKLSGLGLSGSLYYQLSDLSSLTTLDLSNNNIQGNIPYALPQK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 SGT------ NINSVGSGSNINVVSGNDNTVVSGNINHVSG------ 188
                                                                                  ----NNSVGSGSNNVVSGNDNTVVSGNNNHVSG------ 188
                                                                                                                                                                                                                                       -----SDNTVVGSNHVV---SGTKHIVTDNNNVVSGNDNN 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 -SWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 LKSLTTDSOSLGMGSI----NM-----LLH-------VSSRRTLDEEPNTI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :
TONLPOSFSSLSSLSVLYLONNOL-AGSVNVLANLPLTDLNIENNRFSGWVPNAWRSNON 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 ----SGTKHIVTG-----SDNTVVGSNHVV---SGTKHIVTDNNNVVSGNDNN 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GGNSNK 286
119 LQELNLASNGLS-GTIPYSISNMTGLTDLKLSHNQLSGQIQDIFGQLSSLSTLDLSFNTL 177
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                                                                                                                            9 CMLLVFLGFILQVA---GATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWS--GASCC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
12.3%; Score 170.5; DB 4; Length 707;
Best Local Similarity 26.1%; Pred. No. 8.9e-08;
Matches 81; Conservative 39; Mismatches 89; Indels 101; Gaps
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                                                                                                                                                                                                                                       189 ----SINVITVVIG----
                                                                                                                                                                                                                                                                                                                                                                                                    229 VSGSFHTVSG 238
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                                                                                  157 SGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 KŚLŚGGAIVĠ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 KSLSGGAIVG 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-10-101-464A-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-101-464A-80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178
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154 NTISGTNNSVGSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKH 213
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Sequence 7, Application US/09952267B

Patent No. 6733417

GENERAL INFORMATION:

APPLICANT HANSEN. ERIC J.

APPLICANT COPE, LESLIE D.

APPLICANT COPE, LESLIE D.

APPLICANT FISKE, MICHAEL J.

APPLICANT: PISKE, MICHAEL J.

APPLICANT: FREDENBURG, ROSS A.

TITLE OF INVENTION: USPAI AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS

FILE REFERENCE: AMCY:024

CURRENT APPLICATION NUMBER: US/09/952,267B

CURRENT PILING DATE: 1001-09-12

FRIOR FILING DATE: 1999-06-21

NUMBER OF SEQ ID NOS: 98

SOFTWARE: PATENT NOS: 98

SOFTWARE: PATENT NOS: 98

SEQ ID NO 7

LENGTH: 624
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US-10-101-464A-732

US-10-101-464A-732

Sequence 732, Application US/10101464A

Fatent No. 6768041

GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 10000-1020202

CURRENT APPLICATION NUMBER: US/10/101,464A

FILE REFERENCE: 10000-10202

CURRENT FILING DATE: 2002-01-01

FRIOR APPLICATION NUMBER: 09/704,302

FRIOR FILING DATE: 1999-01-12

FRIOR PILING DATE: 1999-01-12

FRIOR APPLICATION NUMBER: 60/162,866

FRIOR FILING DATE: 1999-11-01

FRIOR APPLICATION NUMBER: 60/162,866

FRIOR APPLICATION NUMBER: 60/162,866

FRIOR APPLICATION NUMBER: 09/201-01-01

FRIOR APPLICATION NUMBER: 09/21/US00/00724

FRIOR APPLICATION NUMBER: 03/01-01-01

FRIOR APPLICA
214 IVIDNNNVVSGNDNNVSGSFHTVSGEHNTVS-----GSNNTVSGSNHIVSG---SN 261
                                                                      85 GLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHV- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 RIRGTLSDSLGRLAHLREINVSFNLLTGEVPGRLFL-LQHL--EVLDLSFNNLSVIAPVA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 CNOSDVQALISFKQTVSSSSPLN----WEVNRSCCTWEGVTCGLLSLQQPSVTKLRLPGR 93
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US-10-101-464A-732
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Search completed: May 9, 2005, 20:22:40 Job time : 49 secs

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May 9, 2005, 20:21:56 ; Search time 138 Seconds (without alignments) 645.441 Million cell updates/sec
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1 MPEYMAKCCMLLVFLGFILQ......NTVSGSNHIVSGSNKVVTDG 267
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/cgn2 6/ptodate1/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2 6/ptodate1/2/pubpaa/US10A_PUBCOMB.pep:*
/cgn2 6/ptodate1/2/pubpaa/US10B_PUBCOMB.pep:*
/cgn2 6/ptodate1/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2 6/ptodate1/2/pubpaa/US10C_PUBCOMB.pep:*
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/cgn2_6/prodata/2/pubpaa/US10_TBW PUB.pep.*
/cgn2_6/prodata/2/pubpaa/US11_NBW PUB.pep.*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1428581 seqs, 333598853 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                          OM protein - protein search, using sw model
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                                                     Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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Result No.	Score	% Query Match	% Query Match Length DB	DB	ΩI	Description	
1	262	18.9		16	US-10-437-963-180288	Sequence 180288,	
7	206.5	14.9	1039	16	US-10-437-963-166082	Sequence 166082,	
n	204	14.7		15	US-10-443-101-2	Sequence 2, Appli	
4	198	14.3		16	US-10-437-963-148813	Sequence 148813,	
Ŋ	197	14.2	196	16	US-10-437-963-172660	Sequence 172660,	
9	194	14.0		16	US-10-437-963-115627	Seguence 115627,	
7	194	14.0		16	US-10-437-963-192784	Sequence 192784,	
80	192.5	13.9		16	US-10-437-963-169754	Sequence 169754,	
σ	192	13.9		16	US-10-437-963-153194	Sequence 153194,	
10	190	13.7	1044	16	US-10-437-963-162505	Sequence 162505,	
11	188.5	13.6		16	US-10-437-963-172329	Sequence 172329,	
12	188.5	13.6		16	US-10-437-963-123119	Sequence 123119,	
13	186	13.4		15	US-10-424-599-267766	Sequence 267766,	

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Sequence 153306, Sequence 13619, Sequence 150876, Sequence 150876, Sequence 150876, Sequence 102913, Sequence 102913, Sequence 10294, Sequence 104437, Sequence 110291, Sequence 110398, Sequence 110398, Sequence 114827, Sequence 114827, Sequence 114827, Sequence 114827, Sequence 118391,	Sequence 118888, Sequence 167059, Sequence 158951, Sequence 893, App
100-4337-9963 100-44337-9963	
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676 1012 1013 11133 11140 11241 1065 1080 1080 1080 1081 1080 1081 1081 108	967 1060 344 843
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ALIGNMENTS

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Sequence 180288, Application US/10437963

Sequence 180288, Application No. US20040123343A1

Sequence 180288, Application No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Royal K.

APPLICANT: Shou, Yihua

APPLICANT: Boukharov, Andrey A.

APPLICANT: Brown Andrey A.

APPLICANT: B
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40.1%; Pred. No. 1e-13;
tive 19; Mismatches 53; Indels 34
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Best Local Similarity 40.1%
Matches 71; Conservative
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ORGANISM: Oryza sativa
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Sequence 148813, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
      NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                      Query Match
Best Local Similarity 24.6%
Matches 81; Conservative
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                                                                                        TYPE: PRT
ORGANISM: Daucus carota
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Best Local Similarity
Matches 70; Conserv
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                                                                   LENGTH: 1021
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                            SOFTWARE: 1
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 LTTDSOSLGMGSINMLLHVSSRRTLDEEPNTISGT-----NNSVGSGSNNVVSG 173
                                                                                             -----GGISALLAAVSLRTANLSSNLLNDTLLDLAALPHLSAFNASNNSLSG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 1039;
68 DGVACD-AAARVTALRLPGRGLEGPIPPSLAALARLQDLDLSHNALT--
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Best Local Similarity 29.1%; Pred. No. 6.6e-09;
Matches 83; Conservative 52; Mismatches 103; Indels
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Publication No. US20040096941A1
GENERAL INFORMATION: US20040096941A1
APPLICANT: MATSUBAYASHI, YOSHIKATSU
APPLICANT: SAKAGAMI, YOUJI
TITLE OF INVENTION: RECEPTOR FOR PLANT CELL GROWTH FACTOR
FILE REFERENCE: 238013US0
CURRENT APPLICATION NUMBER: US/10/443,101
CURRENT FILING DATE: 2002-335572
PRIOR FILING DATE: 2002-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT4530_64826C.1.pep
US-10-437-963-166082
                                                                                                                                                                                                             Sequence 166082, Application US/10437963 Publication No. US20040123343A1
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Boukharov, Andrey A.
Barbazuk, Brad
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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APPLICANT:
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APPLICANT: Barbazuk, Brad Applicant: Barbazuk, Brad Applicant: Barbazuk, Brad Applicant: Li, Ping Applicant: Li, Ping Trie OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966
                                                               14;
                                                                                                                                                                                                                                             106
                                                                                                                                                                                                                                                                                      107 GNSLVGEVPKSL----QIRLKSLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISG---- 158
                                                                                                                                                                                                                                                                                                                                                                                                    119 HNSLSGSIAASLLNLSNLEVLDLSSNDFS---GLFPSLINLPSLRVLNVYENSFHGLIPA 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 IGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTV-----SGEHNTVS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 ALONNRLSGA----LSSKLGKLSNLGRLDISSNKFSGKIPDVFLELNKLWYFSAOSNLFN 291
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                                                                                                                                                       8 VILILVGFCVQIVVVNSQNLTCNSNDLKALEGFMRGLESSIDG------WKWNESSS
                                                                                                                                                                                                                                             58 -GASCCSWEGVGCETA-----SGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLS
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                                                                                                                    10 MLLVFLGFILQ--VAGATSWSCHHDDLHAL----RGLAENLSGKGAVRLRAAWS----
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                                                        98;
Length 1021;
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                                                            94; Indels
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US-10-437-963-148813
14.7%; Score 204; DB 15; 24.6%; Pred. No. 1.1e-08; tive 56; Mismatches 94;
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APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Buukharov, Andrey A.

APPLICANT: Ii, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 13-21 [33.21]

CURRENT PILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 115627

LENGTH: 917

TYPE-
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; Sequence 192784, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Brad
APPLICANT: Brad
APPLICANT: Brad
APPLICANT: Application Rice Nucleic Acid Molecules and Other Molecules Associated With
TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 192784
; LENGTH: 1164
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::| ::| |:|| |::| 117 RALDLSANSLSGYLPAALASCGSLVSLNLSGNLLSGPVPDGIWSLPSLRSLDLSGNQLAG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 ---SVPGGFPRSSSLRVLDLSRNLLEGEIPADVGEAGLLKSLDVGHNLFTGELPESLRGL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 WEGVGCETASGRVVALRLPKRGLGGIIP-SSIGELDHLRYLDLSGNSLVGEVPKSLQIRL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 KSLTTDSQSL------GMGSINM-------LLHVSSRRTLDEEPNTISG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 TNNSVGSG------SNNVVSGNDNTVVS-----GNNNHVSGSNNTV--V 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 TGSDNTVVGSNHV-----VSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNTVS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : | | : | | : | | 234 TGLSSLGAGGNALAGELPGWIGEMAALETLDLSGNRFVGAIPDGISGCKNLVE----UD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWS--GASCCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
14.0%; Score 194; DB 16; Length 9
Best Local Similarity 26.3%; Pred. No. 6.8e-08;
Matches 81; Conservative 43; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_19205C.1.pep
US-10-437-963-115627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
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US-10-437-963-192784
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 172660
LENGTH: 961
                                                                                                                                                        61 WEGIAC-GSNGTVTELSLPSMALEGPISVSIANLTGIRRLDLSYNSLSGELPPEL---1S 116
                                                                                                                                                                                                                                      124 SLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSG---SNNVVSGNDNTVVS 180
                                                                                                                                                                                                                                                                           181 GNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTD-NNNVVSGNDNNVSGSFHTVSGE 239
                                                                                                                                                                                                                                                                                                                                                                     67 VGCETASGRVVALRIPKRGLGGIIPSSIGELDHLRYLDLSGN-SLVGEVPKSLQIRLKSL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 TT-----DSQSLGMGSINMLLHVSSRRT-------LDEEPNTISG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 TTLILLGCSFTGDIPEQIGALRQLTFLALNSNKFTGGIPPTLGLLSKLFWLDLSDNQLSG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 THNSVGSGSINNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 -KIPVSSGSN---PGLDQLV---NAEHFHFSENQLTGPIDEKLFSEK---MNLIHVIFDN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MONILILIEMILVSIRISFSQTNPQDVSALQALMKNWQNE-----PQSWMGSTDPCTSWDG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 14.2%; Score 197; DB 16; Length 9 Best Local Similarity 29.5%; Pred. No. 4e-08; Matches 82; Conservative 38; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT4530_70775C.1.pep
US-10-437-963-172660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 NNV---VSGNDNNVSGSFHTVSGEHNTVSGSNNTVSGS. 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 172660, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Gosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-10-437-963-115627
; Sequence 115627, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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221 -RVLKASNNEINGS 233
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ORGANISM: Oryza sativa
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Burkharov, Andrey A.
APPLICANT: Burkharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8 L
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 153194
LENGTH: 1060
     127 IDSOSLGMGSINMLLHVSSRRTLDEEPNTISGINNSVGSGSNN-----VVSGNDNTVVS 180
                                          346 ----IFSGSIVV-----LDVSFNRLGGELQEVDSSSSDWPLQVLNISSNLFTGAF 391
                                                                                                                                              63 SWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 VSGNN--NHVSGSNNTVVTGSDNTVVGSNHVVSG------TKHIVTDNNNVVSGN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 VSGNSFAGHVDAAALCGASPGLRTLRLSMNGFSGDFPVGFGQCRSLVELSLDGNAIAGAL 244
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                                                                                                                                                                                                                                                      452 RMLKAGHNNISGALPDDLFHATSLEY--LSFPNNGLQGTIKLVIKLSNLVFLD 502
                                                                                                                                                                                                                     225 ----NDNNVSGS----FHTVSGEHNTVSGSNNTVSGS-NHIVSGSNKVVTD 266
                                                                                                             181 GNNNHVSGSNNTVVTGSDNTVVG---SNHVVSGTKHIVTD-----NNNVVSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.9%; Score 192; DB 16; Length 1 Best Local Similarity 27.5%; Pred. No. 1.2e-07; Matches 72; Conservative 44; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT4530_53170C.1.pep
US-10-437-963-153194
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 153194, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 DNNVSG--SFHTVSGEHNTVSG 245
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; Sequence 169754, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
    APPLICANT: LA ROSA, Thomas J.
    APPLICANT: Cao, Yongwei
    APPLICANT: Cao, Yongwei
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Bucharov, Andrey A.
    APPLICANT: Li, Ping
    APPLICANT: Li, Ping
    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    CURRENT APPLICANTON NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169754
                                                                                                                                                                                                                                                                                                                                                   65 EGVGCETASGRVVALRIPKRGLG----GIIPSSIGELDHIRYLDLSGNSLVGEVPKSLQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNTVVGSNHVVSG--TKHIVTD-NNNVVSGNDNNVSG-----SFHTVSGEHN----- 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         622 LCASPVKVLRFSANAFSGDVPAGFGQCKLLNDLFLDGNGLTGSLPKDLYTIPELRWLSLQ
                                                                                                                                                                                                                                        8 CCMLLVFLG---FILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
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                                                                                                                              14.0%; Score 194; DB 16; Length 1164; 25.7%; Pred. No. 9.2e-08; tive 38; Mismatches 111; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 838;
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13.9%; Score 192.5; DB 16; Length
Best Local Similarity 28.3%; Pred. No. 8.1e-08;
Matches 83; Conservative 37; Mismatches 106; Indels
                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_88983C.1.pep
US-10-437-963-192784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT4530_68143C.1.pep
US-10-437-963-169754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 -----TVSGSNNTVSGS------NHIVSGSN 261
                                                                                                                              Query Match
Best Local Similarity 25.7%
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Oryza sativa
ORGANISM: Oryza sativa
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APPLICANT: Li, Fing
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)B
CURRENT APPLICATION NUMBER: US,10/437,963
CURRENT FILLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
12;
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                                                                                                                                                                                                                                                                            171 VSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVS 230
                                                                                                                                                                                                                                                                                                                                                                                170 --SNLTTLV----KPIIETN--PIDGKDLSWMGN---LTSLTHFVLEGNRFT----GNIP 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 PAPVICOWTGVSCNNRRHPGRVTTLRLSGAGLVGTISPQLGNLTHLRVLDLSANSLDGDI 117
                                                                                                                                                                                                                                             115 PKSL----QIRLKSLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 VGCETA---SGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPK----- 116
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                                                                                               57
                                                                             4 MISLITHALLLOTVISQTINGDDLSAL----LSFKSLIRDDPREVMSSWDIAGNGINM
                                                                                                                                                61 ----CCSWEGVGCETA--SGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEV
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                                                11 LLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVR-----LRAAWSGAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67; Gaps
  49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 1078;
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  88; Indels
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US-10-437-963-123119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.6%; Score 188.5; DB 16; Best Local Similarity 28.5%; Pred. No. 2.5e-07; Matches 76; Conservative 32; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(1078)
OTHER INFORMATION: unsure at all Xaa locations
  32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 123119, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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Barbazuk, Brad
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
  74; Conservative
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ORGANISM: Oryza Bativa
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US-10-437-963-123119
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NAME/KEY: ungure
LOCATION: (1)..(
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APPLICANT:
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  Matches
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                                                                APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 162505
LENGTH: 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Li, Fing
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILMG DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 172329
LENGTH: 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 GASC--CSWEGVGCETASG--RVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 VPKSL----QIRLKSLITDSQSLGMGSINMLL-HVSSRRTLDEEPNTISGTNNSVGSG-- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 IPSELGHLGQISYLNL-----SINSLEGHIPDELSLCSKLKVLSLCNNSLQGEIP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 -----SINNVSGNDNT----VVSGNNNHVSGSNNTVVTGSDNTV-- 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 PSLTQCTHLQQVVLCNNKLQGRIPTKFGMLHELKTLDLSNNALTGDIPPLLGSSPSFVYV 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 -VGSNHVVSGTKHIVTDNNN--VVSGNDNNVSGSFHTV---SGEHNTVSGSNNTVSGS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MPEYMAKCCMLLVFLG-PILQVAGATSWSCHHD-DLHALRGLAENLSG-KGAVRLRAAWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
13.7%; Score 190; DB 16; Length 10
Best Local Similarity 26.5%; Pred. No. 1.8e-07;
Matches 79; Conservative 47; Mismatches 114; Indels
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US-10-437-963-172329
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US-10-437-963-162505
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                                              Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boukharov, Andrey A.
Barbazuk, Brad
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30.5%;
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
  Cao, Yongwei
Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Oryza sativa
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Best Local Similarity
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US-10-437-963-172329
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APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 192786
LENGTH: 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 S--CCSWEGVGCETASGRVVALRLPKRGLGGIIP-SSIGELDHLRYLDLSGNSLVGEVPK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 SLOIRLKSLTTDSQSLGMGSINM---LLHVSSRRTLDEEPNTISGTNNSVGSGSNNVVSG 173
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                                                                                                                                                                                                                                                                                                                                                                                                           1 MPEYMAKCCMLLVFLGFILQVAGATSWSCHHDDLHALR-GLAENLSGKGAVRLRAAWSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPPPRLPCLAAFLALALVVVCAA-----EPDADRAALLDFLAGLGGGRGRINWASS
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13.4%; Score 185; DB 16; Length 1012;
Best Local Similarity 25.6%; Pred. No. 4.6e-07;
Matches 87; Conservative 35; Mismatches 116; Indels 102
                                                                                                                                                                                                                                                                                                              Length 676;
                                                                                                                                                                                                                                                                                                                                                              98; Indels
                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_53274C.l.pep
US-10-437-963-153306
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US-10-437-963-192786
                                                                                                                                                                                                                                                                                                       13.4%; Score 186; DB 16;
30.4%; Pred. No. 2.3e-07;
tive 30; Mismatches 98;
                                                                                                                                                        LOCATION: (1)..(676)
OTHER INFORMATION: unsure at all Xaa locations
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; Sequence 192786, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.4%;
                                                                         ORGANISM: Oryza sativa
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                                                                                                    FEATURE: NAME/KEY: unsure
SEQ ID NO 153306
LENGTH: 676
                                                    TYPE: PRT
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                           Sequence 267766, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La ROSa Thomas J
APPLICANT: La ROSa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 GEVPKSLQIRLKSL-----TTDS----QSLGMGSINMLLHVSSR---- 146
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| SRIPEDF-ANLKSLRNLYLQGNFFSGEVSDSVFALQNLVRLNLGNNNFSGEISPKFNSLT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 -----ASCCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MPEYMAKCCMILLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSG-- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKSARVKEAILLVFMFSLLSIA-----C--SDLASDRA-----GLLLLRSAVGGRT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 RLATLYLERNNFTGSIPDLDAPPLDQFNVSFNSLTGSIPNRFSRLDRTAPLGNS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TINNSVGSGSNNVVSGNDNTVVSGNN 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.4%; Score 186; DB 15; Length 278; Best Local Similarity 30.3%; Pred. No. 7.2e-08; Matches 71; Conservative 23; Mismatches 70; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_83815C.1.pep
US-10-424-599-267766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)..(278)
OTHER INFORMATION: unsure at all Xaa locations
                     195 TGSDNTVVGSNHVVSGTKHIVTDNNNV 221
                                                         241 TGE---LPGELFDVKALQHLELPANOI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 153306, Application US/10437963;
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovallc, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Roy Youwei
APPLICANT: Wu, Wai
APPLICANT: Wu, Wai
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 --RTLDEEPNTISG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                     US-10-424-599-267766
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LOCATION: (1)..(
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LENGTH: 278
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120 IRLKSLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNT-- 177

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2GPPAIR-VVNVSSNGFTGPHPAFPGAPNITVLDITGNAFSGGINVTA 167	8VVSGNNHVSGS 197	168 LCASPVKVLRFSANAFSGDVPAGFGQCKLLNDLFLDGNGLTGSLPKDLYMMPALRKLSLQ 227	198 DNTVVGSNHVVSGTKHIVTDNNNVVSGNNVSGSFHTVSGEHN 241	228 ENKLSGSLDDDLGNLTEITQIDLSYNMFNGNIPDVFGKLRSLESLNLASNQLNGTLPLSL 287	TVSGSNNTVSGS	288 SSCPMLRVVSLRINNSLSGEITIDCRLLTRLNNFDAGTNKL 327
122	178	16	19	22	242	28
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Search completed: May 9, 2005, 20:34:42 Job time : 144 secs

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9, 2005, 20:10:27 ; Search time 73 Seconds (without alignments) 1414.589 Million cell updates/sec
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1 MPBYMAKCCMLLVFLGFILQ.......NTVSGSNHIVSGSNKVVTDG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                   2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp1990s:*
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Maximum DB seq length: 200000000
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                                                                                                                  May
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003as:*
geneseqp2003bs:*

	Description	Adm41473 Perennial	Adm41474 Tall fesc	Adm41481 Tall fesc	Adm41480 Perennial	Adm41482 Perennial	Adm41477 Perennial	Adm41476 Tall fesc	Adm41483 Perennial	Adm41475 Perennial	Adm41479 Tall fesc	Adm41478 Perennial	Adm41472 Tall fesc	Adm41471 Perennial			-		-	Abb93984 Herbicida	Adn72587 Thale cre		Adj49621 Oil-assoc	m	Aag32217 Arabidops	Aag32216 Arabidops
SUMMARIES	ai	ADM41473	ADM41474	ADM41481	ADM41480	ADM41482	ADM41477	ADM41476	ADM41483	ADM41475	ADM41479	ADM41478	ADM41472	ADM41471	AAY22472	ABB93804	AD014158	AAG20654	AAG20653	ABB93984	ADN72587	AAW68205	ADJ49621	AAW68203	AAG32217	AAG32216
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	* Query Match Length	267	269	262	254	256	277	277	281	281	285	280	243	243	118	1036	1021	598	599	751	1008	941	653	892	735	743
	% Query Match	100.0	93.1	71.7	70.8	70.3	65.7	65.6	65.3	65.1	65.1	63.8	48.2	47.3	38.3	18.7	14.7	14.3	14.3	14.3	13.8	13.1	13.1	12.8	12.7	12.7
	Score	1385	1290	992.5	980.5	973.5	910.5	908.5	904.5	901.5	901.5	884	668	655	530	258.5	204	197.5	197.5	197.5	190.5	182	181	177	176.5	176.5
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AAB25515	ABU34968	AAW68208	AAB25518	ABB91206	AAB25445	AAB25527	AAB25112	AAW68204	AAB25413	ABB91562	ADQ36979	ADQ15649	ABB93915	ADI32622	AAM42228	AAM42230	AAM42232	ABB92188	ADN72847
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804	852	889	843	290	323	386	707	624	187	1095	938	938	996	996	854	854	854	627	627
12.7	12.7	12.6	12.6	12.5	12.4	12.3	12.3	12.3	12.2	12.2	12.0	12.0	12.0	12.0	11.9	11.9	11.9	11.9	11.9
176.5	176	175	174	173.5	171.5	170.5	170.5	170	168.5	168.5	166.5	166.5	166	166	165.5	165.5	165.5	165	165
26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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/note="Conserved leucine-rich repeats"
152. .266
/note= "7-amino acid sequence repeat region identified in antifreeze proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted biocrystals (e.g. gout).
                                                                                                                                                                                                                 /note= "Conserved Cys pairs identified N-terminal of leucine-rich repeats of receptor-like kinases"
                                                                                                     Antifreeze, perennial ryegrass; cold tolerance; transgenic; plant; antigout; litholytic; nephrotropic; cytostatic.
                                                                                 Perennial ryegrass antifreeze protein AFP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hall C, Fish SA;
                                                                                                                                                                                1. .23
/label= Signal_peptide
                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD. (WRIG-) WRIGHTSON SEEDS LTD.
       ADM41473 standard; protein; 267 AA.
                                                                                                                                                                                                                                                                                                                                                                 09-SEP-2003; 2003WO-NZ000199
                                                                                                                                                                                                                                                                                                                                                                                        09-SEP-2002; 2002US-0409557P
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Demmer J Shenk MA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADM41460
                                                                                                                                                                                                                                                                                                                  WO2004022700-A2.
                                                                                                                                            Lolium perenne.
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                                                         03-JUN-2004
                                  ADM41473;
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Peptide
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ADM41473
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Misc-difference 124
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                                   The present sequence is that of AFP2, an antifreeze protein of perennial ryegrass. The encoding cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymuclocitides can coding them ADM41458-ADM41483. The polymuclectides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymuclectides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymuclectide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded CRNA corresponding to the polymuclectide into the cells of the organism, antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and control can patient e.g. tumour tissue, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKSLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fescue; cold tolerance; transgenic; plant; antigout;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1385; DB 8; Length 267; 100.0%; Pred. No. 5.4e-114; ive 0; Mismatches 0; Indels 0;
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/note= "Conserved leucine-rich repeats"
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1. .24
1. dabel= Signal_peptide
61. .72
/note= "Conserved Cys pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          litholytic; nephrotropic; cytostatic.
Claim 7; SEQ ID NO 16; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 267; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 267 AA;
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The present sequence is that of an antifreeze protein of tall fescue. The encoding cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegass and tall fescue)

cutifreeze proteins and the polymucleotides encoding them ADMA1458-

ADMA1483. The polymucleotides were isolated from tissues taken at the plants. The polymucleotides were isolated from different parts of the plants. The polymucleotides can be used to modulate the cold to the plants. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism to the cold additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kindey stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient of the control of the con
                                                                   154. 268 //note= "7-amino acid sequence repeat region identified in
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Pred. No. 1.4e-105;
6; Mismatches 10;
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'note= "Encoded by TAG
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                                                                                                                                                                                                                           antifreeze proteins"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hall C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-SEP-2003; 2003WO-NZ000199.
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Matches 251; Conserv
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM41480 standard; protein; 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hall C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39-SEP-2003; 2003WO-NZ000199
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       frost or freezing.
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                                                    Sequence 262 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of an antifreeze protein of tall fescue. The encoding cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41458-C different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "7-amino acid sequence repeat region identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        patient e.g. tumour tissue, and to protect a plant from damage due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Conserved Cys-pairs identified N-terminal leucine-rich repeats of receptor-like kinases"
                                                                                                                                                                                                                                                                                                                             Antifreeze, fescue, cold tolerance, transgenic, plant, antigout,
litholytic, nephrotropic, cytostatic.

    114
    /note= "Conserved leucine-rich repeats"
    147. .261

Fish SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .23
/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antifreeze proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENESIS RES & DEV CORP LTD.
                                                                                                                                             ADM41481 standard; protein; 262 AA
                                                                                                                                                                                                                                                                             Tall fescue antifreeze protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (WRIG-) WRIGHTSON SEEDS LTD
                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  Schedonorus arundinaceus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57. .68
/note= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biocrystals (e.g. gout).
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N-PSDB; ADM41468.
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                          241
                                                                                                                                                                                         ADM41481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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                                                                                                                ADM 11481

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 WEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLK 123
                                                                                                                                                                                                                                                                                                                                                   124 SLITIDSQSLGMGSINMLLHV-SSRRILDEEPNTISGINNSVGSGSNNVVSGNDNTVVSGN 182
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                                                                                                                                                                        9
                                                                                                                     63
                                                                                                                     5 MAKCCMLLVFLGFILQVAG-ATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCS
                                                                                                                                                                        1 MAKCIMILISFAFILISAAGTATATPCHRDDLRALRGFAENIGGGGALSLRAAWSGASCCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 NNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNT
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57. 68
/note= "Conserved Cys-pairs identified N-terminal or
leucine-rich repeats of receptor-like kinases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antifreeze, perennial ryegrass; cold tolerance; transgenic; plant; antigout; litholytic; nephrotropic; cytostatic.
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                                                            5
   Length 262;
                                                            Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Conserved leucine-rich repeats"
Query Match 71.7%; Score 992.5; DB 8; Best Local Similarity 75.0%; Pred. No. 2.8e-79; Matches 198; Conservative 22; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perennial ryegrass antifreeze protein AFP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fish SA;
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 VSGSNNTVSGSNHVVSGSNKVVTD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antifreeze proteins"
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The present sequence is that of AFP5, an antifreeze protein of perennial ryegrass. The encoding cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall feacue) antifreeze proteins and the polymucleotides encoding them ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides were isolated from condulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter. Sequence, into the genome of the organism, or introducing double-stranded CR NNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze protein can be used for the cryopresservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a contour and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 WEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 MAKCCMLLVFLGFILQVAG-ATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 SLTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNT
modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.8%; Score 980.5; DB 8; Length 254; Best Local Similarity 73.5%; Pred. No. 3e-78; Matches 194; Conservative 24; Mismatches 33; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antifreeze; perennial ryegrass; cold tolerance;
antigout; litholytic; nephrotropic; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSGSNNTVSGSNHVVSGSNKVVTD 253
                                                                            Claim 7; SEQ ID NO 23; 71pp; English.
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                                           biocrystals (e.g. gout).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 254 AA;
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                     treating
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The present sequence is that of an antifreeze protein of perennial ryegrass. The encoding cDNA was isolated from a leaf and pseudostem CDNA expression library. The invention provides forage grass (perennial recoins and tall fescue) antifreeze proteins and the polymucleotides corrected and tall fescue) antifreeze proteins and the polymucleotides corrected from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides were isolated from different parts of the plants. The polymucleotides can be used to manifreeze polymucleotide, under the control of a gene promoter conterpoint into the genome of the organism, or introducing double-stranded sequence, into the genome of the organism, or introducing double-stranded conterpoint inhibiting expression of an antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a clisor characterised by biocrystals associated with disorders such and kidney stones, tone them a patient e.g. tumour tissue, and crease the content of the plants and the content of the content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CDWEGYGCDGASGRYTALWLPRSGLTGPIPSWIFQLHHLRYLDLSGNALYGEVPRXLQVQ 120
                                                                                                                          /note= "7-amino acid sequence repeat region identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
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     ò
/note= "Conserved Cys-pairs identified N-terminal leucine-rich repeats of receptor-like kinases"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to protect a plant from damage due to frost or freezing.
                                                                         /note= "Conserved leucine-rich repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fish SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; SEQ ID NO 25; 71pp; English.
                                                                                                                                                         antifreeze proteins"
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Best Local Similarity 72.6%
Matches 193; Conservative
                                                                                                      .255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Demmer J, Shenk MA,
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N-PSDB; ADM41469.
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                                                          Region
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170

1. .23 /label= Signal_peptide

Location/Qualifiers

Lolium perenne

Peptide Region ů

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patient e.g. tumour tissue, and to protect a plant from damage due
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            frost or freezing
                                    Sequence 277 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tall fescue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antifreeze;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                litholytic;
                                                                                                                                                                                                                                                                                                                                                                                                                         ADM41476;
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ADM41476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypetide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to a frozen food product, or treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a
                                                                                                                                                                                                                                                                                                                                                                         /note= "7-amino acid sequence repeat region identified in antifreeze proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of APP3, an antifreeze protein of perennial ryegrass. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41483-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                          /note= "Conserved Cys pairs identified N-terminal of leucine-rich repeats of receptor-like kinases"
                                                                                                                                                                                                transgenic; plant;

    125
    note= "Conserved leucine-rich repeats"

                                                                                                                                                                                               Antifreeze, perennial ryegrass, cold tolerance, antigout, litholytic, nephrotropic, cytostatic.
          Fish SA;
                                                                                                                                                                                                                                                                        1. .23
/label= Signal_peptide
                                                                                                                                                                      Perennial ryegrass antifreeze protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; SEQ ID NO 20; 71pp; English.
                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                               ADM41477 standard; protein; 277 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENESIS RES & DEV CORP
WRIGHTSON SEEDS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hall C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-2002; 2002US-0409557P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-SEP-2003; 2003WO-NZ000199
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                            161. .275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biocrystals (e.g. gout).
                                                                                                                                                                                                                                                                                              .64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-248453/23
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                                                                                                                                                                                                                                   Lolium perenne
                                                                                                                                              03-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Demmer J,
                                                                                                                        ADM41477;
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                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                 177
                                                                                                                                                                                                                                                                                                                                                             65 EGVGCETASGRVVALRLP------KRGLGGIIPSSIGELDHLRYLDLSGNS 109
                                                                                                                                                                                                                                                     110 LVGEVPKSLOIRLKSLTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSN 168
                                                                                                                                                                                                                                                                                                                                     169 NVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNN 228
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                                                                                                                                                                                                                                                                             1 MAKCWILILIELVFILLAVCAT--SCHPDDIRALRGFVGNLNG-GGVILRETWSGSSCCAW
                                                                                    5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
                                             Gaps

    53. .64
    7 hote= "Conserved Cys-pairs identified N-terminal
leucine-rich repeats of receptor-like kinases"
69. .124

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                                             19;
    Length 277;
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Conserved leucine-rich repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                          229 VSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                             238 VSGSFHTVSGSHNTVSGSNNTVSGSNHVVSGSNKVVT 274
                                             51;
  DB 8;
; Score 910.5; DB 6; Pred. No. 5.3e-72; 20; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fish SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .22
'label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADM41476 standard; protein; 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antifreeze protein.
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  Query Match
Best Local Similarity 67.5%;
Matches 187; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schedonorus arundinaceus
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/note= ".
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interest proteins and the polynucleotides encoding them ADM41459-
antifreeze proteins and the polynucleotides encoding them ADM41459-
ADM41483. The polynucleotides were isolated from tissues taken at
different times of year (winter and spring) and from different parts of
the plants. The polynucleotides can be used to modulate the cold
to clerance of an organism, especially plants, mammals, insects, fungi,
carchaea and bacteria. The method involves incorporating an antifreeze
to polynucleotide, under the control of a gene promoter sequence, into the
copynucleotide into the cells of the organism, thereby inhibiting
to the polynucleotide into the cells of the organism, thereby inhibiting
expression of an antifreeze polypeptide. The antifreeze protein can be
cused for the cryopreservation of a cell or tissue, as a food additive of
a frozen food product, in a method for decreasing the time required to
chehydrate a composition, to treat a disorder characterised by biocrysteals
cassociated with disorders such as gout and kidney stones, to preserve the
viability of a molecular biology reagent, to destroy unwanted tissue in a
copy frage or freeding the plant from damage due to
                                            New antifreeze proteins and encoding polymucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                          present sequence is that of an antifreeze protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.6%; Score 908.5; DB 8;
67.9%; Pred. No. 8e-72;
Migmatches 51;
                                                                                                                                                                      Claim 7; SEQ ID NO 19; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 67.99
Matches 188; Conservative
                                                                                                                       biocrystals (e.g. gout)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rost or freezing
N-PSDB; ADM41463
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                                                                                                                                     5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
                                                                         EGVGCETASGRVVALRLP-------KRGLGGIIPSSIGELDHLRYLDLSGNS
                                                                                                                                                                         110 LVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSN
DB 8; Length 277;
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                                                                                                                                                                                                                                                                                                                238 VSGSSHTVSGSHNTVSGSNHVVSGSNHVVSGSNKVVT 274
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transgenic; plant;
                                                                                                Antifreeze, perennial ryegrass; cold tolerance; antigout; litholytic; nephrotropic; cytostatic.
                                                                             Perennial ryegrass antifreeze protein.
                   ADM41483 standard; protein; 281 AA
                                                          (first entry)
                                                                                                                              Lolium perenne
                                                          03-JUN-2004
                                        ADM41483;
RESULT 8
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Location/Qualifiers 1.19

Key Peptide

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The present sequence is that of an antifreeze protein of perennial ryegrass. The invention provides forage grass (perennial ryegrass and tayegrass. The invention provides forage grass (perennial ryegrass and tall feature) antifreeze proteins and the polymucleotides encoding them ADM41458-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold to learned of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze of polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the control of the control of the description of a sesociated with disorders such as gout and kidney stones, to preserve the control of the cont
                                                                                                                                                                                                    'note= "7-amino acid sequence repeat region identified in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
                                          "Conserved lipoprotein membrane attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGVGCETASGRVVALRLP------KRGLGGIIPSSIGELDHLRYLDLSGNS
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                                                                                  note= "Conserved Cys-pairs identified N-terminal eucine-rich repeats of receptor-like kinases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
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                                                                                                                                                       "Conserved leucine-rich
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66.5%; Pred. No. 1.8e
ive 20; Mismatches
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Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; SEQ ID NO 26; 71pp; English.
                                                                                                                                                                                                                            antifreeze proteins"
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                                                                                                                                                                                                                                                                                                                                                              09-SEP-2003; 2003WO-NZ000199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENESIS RES & DEV C(WRIG-) WRIGHTSON SEEDS LTD
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Best Local Similarity 66.5%;
Matches 187; Conservative
                                                                                                                                                                               .279
label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating tumors or disobiocrystals (e.g. gout)
                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Demmer J, Shenk MA,
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RESULT 10
ADM41479
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/note= "7-amino acid sequence repeat region identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of APP3, an antifreeze protein of perennial ryegrass. The encoding cDNA was isolated from a root cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) attifreeze proteins and the polynucleotides encoding them ADM41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting
224
                    237
                                                                                                                                                                                                                                                                                                     "Conserved lipoprotein membrane attachment site"
 SGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSG
            New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                       transgenic; plant;
                                                                                                                                                                                                                                                                                                                        /note= "Conserved Cys-pairs identified N-terminal leucine-rich repeats of receptor-like kinases"
                                                                                                                                                                                                                                                                                                                                                         /note= "Conserved leucine-rich repeats"
                                         265
                                                   Antifreeze, perennial ryegrass, cold tolerance, antigout, litholytic, nephrotropic, cytostatic.
                                                                                                                                                                                  Perennial ryegrass antifreeze protein AFP3.
                                                                                                                                                                                                                                                                      1. .19
/label= Signal_peptide
10. .22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fish SA;
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                                                                                                                                                                                                                                                                                                                                                                                         antifreeze proteins"
                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                  ADM41475 standard; protein; 281
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WRIGHTSON SEEDS LTD.
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                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Demmer J, Shenk MA,
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N-PSDB; ADM41462.
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                    178
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                                                            238
                                                                                                                                        ADM41475;
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                used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to a feedyfarte a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fescue; cold tolerance; transgenic; plant; antigout;
expression of an antifreeze polypeptide. The antifreeze protein
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                                                                                                                                                                                                                                                    Length 281;
                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 NDNNVSGSFHTVSGSHNTVSGSNNTVSGSNHVVSGSNKLVT 278
                                                                                                                                                                                                                                               65.1%; Score 901.5; DB 8; 66.2%; Pred. No. 3.4e-71; ive 21; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Conserved leucine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .17
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nephrotropic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM41479 standard; protein; 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antifreeze protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-2003; 2003WO-NZ000199.
                                                                                                                                                                                                                                                                                            Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schedonorus arundinaceus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52. .63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note =
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                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                            frost or freezing
                                                                                                                                                                                                    Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004022700-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antifreeze;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               litholytic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADM41479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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09-SEP-2002; 2002US-0409557P.

us-10-657-852a-15.rag

Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant; antigout; litholytic; nephrotropic; cytostatic.

ryegrass antifreeze protein AFP4.

Perennial

/note= "7-amino acid sequence repeat region identified in antifreeze proteins"

SA;

Fish

Hall C,

Demmer J, Shenk MA, 2004-248453/23.

N-PSDB; ADM41465.

DEV CORP LTD.

(WRIG-) WRIGHTSON SEEDS LTD

(GENE-) GENESIS RES &

09-SEP-2002; 2002US-0409557P. 09-SEP-2003; 2003WO-NZ000199.

12. .22 /note= "Conserved lipoprotein membrane attachment site" 52. .63

1. .22
/label= Signal_peptide

ocation/Qualifiers

Lolium perenne

Key Peptide Region Region

note= "Conserved Cys-pairs identified N-terminal or eucline-rich repeats of receptor-like kinases"

note= "Conserved leucine-rich repeats"

Transmembrane domain

WO2004022700-A2

18-MAR-2004.

68. .134

Region Domain Region

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The present sequence is that of an antifreeze protein of tall fescue. The encoding cDNA was isolated from a leaf blade cDNA expression library. The encoding cDNA was isolated from a leaf blade cDNA expression library. The convention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADMA1458.

ADMA1483. The polymucleotides were isolated from tissues taken at conferent times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to omodulate the cold cold cold archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the composition of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the patient e.g. tumour tissue, and to protect a plant from damage due to
                                                                                                                                                                               New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                        Fish SA;
                                                                                                                                                                                                                                                                        Claim 7; SEQ ID NO 22; 71pp; English
                                (GENE-) GENESIS RES & DEV CORP LTD. (WRIG-) WRIGHTSON SEEDS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADM41478 standard; protein; 280 AA
                                                                                        Hall C,
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                                                                                                                                                                                                                                       biocrystals (e.g. gout).
                                                                                        Demmer J, Shenk MA,
                                                                                                                           2004-248453/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   frost or freezing
                                                                                                                                           N-PSDB; ADM41466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 285 AA;
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ID ADM4
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AC ADM4
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                                                                                                                                                                         70 ETASGRVVALRIPKRGLG---------GIIPSSIGELDHLRYLD 104
                                                                                                                                                                                                                                                                                            182 LSGRNNVVSGNDNTVISENNNTVSGSFNTVIIGSDNVLTGSNHVVSGRSHIVTDNNNSVS 241
                                                                                                                                                                                                                     62 NGASGRITTLMLPRRGLAGTITGASLAGLARLESLNLANNRLVGTIPSWIGELDHLLYLD 121
                                                                                                                                                                                                                                                                                                                                                     GSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVS 223
                                                                                                69
                                                                                                                                         61
                                                                                    10 MLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSWEGVGC
                                                                                                                Gaps
                                                27;
         DB 8; Length 285;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          GNDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVTDG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.1%; Score 901.5; DB 8; Best Local Similarity 65.5%; Pred. No. 3.5e-71; Matches 186; Conservative 17; Mismatches 54;
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The present sequence is that of AFP4, an antifreeze protein of perennial ryegrass. The encoding cDNA was isolated from a leaf and pseudostem cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymuclectides conding them ADM4158-ADM4183. The polymuclectides were isolated from cirsues taken at different times of year (winter and spring) and from different parts of the plants. The polymuclectides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaed and bacteria. The method involves incorporating an antifreeze polymuclectide, under the control of a gene promoter. Sequence, into the genome of the organism, or introducing double-stranded thereby inhibiting expression of an antifreeze polypeptide. The control of a gene promoter content of the polymuclectide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The control of a gene promoter content of a cold organism, thereby inhibiting expression of an encrypreservation of a cell or decreasing the time required to dehydrate a composition, to treat a disorder characterised by blocrystals associated with disorders such as a cold and the plants and the proposed organism of a matter of disorder characterised by blocrystals associated with disorders such as the plants of the plants in a patient e.g. tumour tissue, and content of the plants. The plants of the plants and plants of the plants and plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from damage due to frost or freezing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; SEQ ID NO 21; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biocrystals (e.g. gout).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to protect a plant
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4

Gaps

32;

Length 280;

63.8%; Score 884; DB 8; Length 280 65.5%; Pred. No. 1.2e-69; ive 14; Mismatches 52; Indels

Query Match
Best Local Similarity 65.5%
Matches 186; Conservative

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rost or freezing
                                                                                                                                                                                                                                                                                                                           Sequence 243 AA;
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ADM41471
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                                                                                                                                                                                                                                                  177 LSGRNWTVSGNDNTVISGNNMTVSGSFNTVVTGSDNVLTGSNHVVSGRNHIVTDNNNAVS 236
                                                                                                                                                                             223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "7-amino acid sequence repeat region identified in antifreeze proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of an antifreeze protein of tall fescue. The encoding CDNA was isolated from a basal stem CDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41458-
                                                                                                              121
                                                                                                                                                 LSGNSLVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHVS-SRRTLDBEPNTISGTNNSV 163
                                                                          ----GIIPSSIGELDHLRYLD 104
 69
                                     61
                                                                                                        NGASGRVTTLWLPRRGLAGTITGASLAGLARLESLNLANNRLVGTIPSWIGELDHLLYLD
                     GSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVS
MLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSWEGVGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Conserved Cys-pairs identified N-terminal or leucine-rich repeats of receptor-like kinases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic; plant; antigout;
                                                                                                                                                                                                                                                                                                                         GNDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVTDG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .. .20
/label= Signal_peptide
                                                                        ETASGRVVALRLPKRGLG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fescue; cold tolerance; to nephrotropic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; SEQ ID NO 15; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADM41472 standard; protein; 243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tall fescue antifreeze protein.
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WRIGHTSON SEEDS LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-SEP-2003; 2003WO-NZ000199.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               litholytic;
                                                                                                              62
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MDW41472

MDW4147
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different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold a trolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antiffreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 LTTAGRSLGKAPTNMPLHVKSSQCTLDEEHNTITGINNTVKSGSNNVVSGNDNTVISGNN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 NHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEH--- 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107. .242
/note= "7-amino acid sequence repeat region identified in
antifreeze proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SFÖILLKG 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAKCWOLLLFLAFILPAASAA - - SRHPDDLRALQDFAGNLRGGGVV - LRAALSGGSCCDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 LTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Indels 64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antifreeze, perennial ryegrass; cold tolerance; transgenic; plant; antigout; litholytic; nephrotropic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53. .64
/note= "Conserved Cys-pairs identified N-terminal
The polynucleotides were isolated from tissues taken at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leucine-rich repeats of receptor-like kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 ------NTVSGSNNTVSGSNHIVSGSNKVVTDG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SASHSTISGNHNTVSGSNNFVSGNNNIVSGSNHVVYGNNKVVTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 668; DB 8;
Pred. No. 1.2e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 48.2%; Score 668; DB Best Local Similarity 53.0%; Pred. No. 1.2e-Matches 151; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perennial ryegrass antifreeze protein AFP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .20
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 EGAĞCDGASGRVT----
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/note= "
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18-MAR-2004

us-10-657-852a-15.rag

AAY22472;

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The present sequence is that of APP1, an antifreeze protein of perennial ryegrass. The encoding CDNA was isolated from a pseudostem CDNA corpression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides corpression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter of sequence into the genome of the organism, or introducing double-stranded RNA corresponding to the plants of the organism, or thereby inhibiting expression of an antifreeze polypeptide. The classe, as a food additive of a frozan food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the patient e.g. tumour tissue, and control can patient e.g. tumour tissue, and control can patient e.g. tumour tissue, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 NHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNTV 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLKS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LITDSQSLGMGSINMLLHVS-SRRTLDEEPNTISGINNSVGSGSNNVVSGNDNTVVSGNN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGVGCDGASGCV------kSPQILLKG 78
                                                                                                                                                                                                                                                                             New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 SGSHSTVSGNHNTVSGRNNSVYGNNNIVSGSNHVVYGNNKVVTGG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.3%; Score 655; DB 8;
51.9%; Pred. No. 1.8e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Mismatches
                                                                                                                                                                              Demmer J, Shenk MA, Hall C, Fish SA,
                                                                                                                                                                                                                                                                                                                                                                              Claim 7; SEQ ID NO 14; 71pp; English.
                                                                                                                  (GENE-) GENESIS RES & DEV CORP LTD (WRIG-) WRIGHTSON SEEDS LTD.
                                     09-SEP-2003; 2003WO-NZ000199.
                                                                              09-SEP-2002; 2002US-0409557P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                         biocrystals (e.g. gout).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                 WPI; 2004-248453/23.
N-PSDB; ADM41458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 243 AA;
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AAY22472
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AAY22472 standard; protein; 118 AA.

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This sequence is the plant anti-freeze protein of the invention. The anti-freeze protein is characterised in that at least 40% of its amino acids are from the group of serine, threonine and apparagine. The amino acids protein can be used in frozen food products, especially frozen confectionery. Anti-freeze proteins are especially infood products, which are heated, e.g. by pasteurisation, blandhing or sterilisation prior to freezing. Plants transformed with a nucleic acid sequence encoding the anti-freeze protein have an increased frost tolerance. Prior at anti-freeze proteins have not been applied to commercially available food products, due to high costs and complicated processes for obtaining the protein. Also prior art anti-freeze proteins have tended to commercially available for destabilise during processing especially during the pasteurisation step. This is overcome by the present anti-freeze protein. The anti-freeze protein ingredient means that mixes can be frozen under quiescent conditions, e.g. in a shop or home freezer without the formation of unacceptable ice crystal shapes and home freezer without the formation of unacceptable ice crystal shapes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 DEEPNTISGINNSVGSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVS 209
                                                                                                Anti-freeze protein; grass; plant; frozen food product; frost tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 GTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVTD 266
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New plant anti-freeze protein useful in frozen food products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.3%; Score 530; DB 2; Length 11
85.5%; Pred. No. 7.3e-39;
ive 10; Mismatches 7; Indels
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                                                               Grass anti-freeze protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 36; 39pp; English
                                                                                                                                                                                                                                                     98WO-EP008553.
                                                                                                                                                                                                                                                                                   98GB-00001408
                                                                                                                                                                                                                                                                                                                                                                      Jarman CD, Sidebottom CM,
                               29-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 100; Conservative
                                                                                                                   frozen confectionery
                                                                                                                                                                                                                                                                                                                     (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-458697/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quiescent freezing
                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX99717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 118 AA;
                                                                                                                                                 Lolium perenne.
                                                                                                                                                                                                                                                                                     22-JAN-1998;
                                                                                                                                                                                                                                                    23-DEC-1998;
                                                                                                                                                                                   WO9937782-A2
                                                                                                                                                                                                                    29-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB93804;
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ID ABBS
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53; Gaps 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 LDL---SHNLLSGSVLGVVSGLKILQSLNISSNSLSGKLSDVGVPPGLVMLNVSNNLFEG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CE--TASGRUVALRIPKRGIGGIIPSSIGELDHIRYLDISGNSLVGEVPKSL---QIRL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 NDNTVV----SGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSG----- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 EIHPELCSSSGGIQVLDLSMNRLVGNLD----GLYNCSKSIQQLHIDSNRLTGQLPDYLY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 MLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAW-SGASCCSWEGVG 68
                                                                                                                                                                                                                                                                                                                                                                                                                 comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                Identifying plant target proteins for herbicidally active compounds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 SIRELEQLSLSGNY--LSGE---LSKNLSNLSGLKSLLISENRFSDVIPD 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----NDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNK----VVTD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
18.7%; Score 258.5; DB 5; Length 1036;
Best Local Similarity 30.7%; Pred. No. 1.6e-13;
Matches 89; Conservative 50; Mismatches 98; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; SEQ ID NO 3015; 261pp + Sequence Listing; English.
                 Herbicidally active polypeptide SEQ ID NO 3015.
                                                      Herbicidal; plant; agriculture; herbicide.
                                                                                                                                                                                                        28-AUG-2001; 2001WO-EP009892.
                                                                                                                                                                                                                                             28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                                                    Tietjen K, Weidler M;
                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-269010/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1036 AA;
                                                                                                                                                                                                                                                                                 (FARB ) BAYER AG.
                                                                                                                            WO200210210-A2
                                                                                                                                                                 07-PEB-2002
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BJ460799 BJ456413 BJ447068 BJ4502087 BJ4502087 BJ3602087 BJ3603087 BJ360308 BJ360308 BJ45358 BJ45358 BJ45358 BJ45358 BJ45358 BJ45358 BJ45358 BJ453528 BJ4535	ALIGNMENTS	B1451048 B4451048 B4451048 B4451048 B4451048 B451048 B	Score 372.8 Pred. No. 4 0; Mismatch	AGCGGCCGCG TCGCATGGT
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FEATURES

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/dev_stage="vegetative stage"
/clone_lib="K. Sato unpublished cDNA lakashinrik vegetative stage leaves"
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llarity 73.7%; Pred. No. 5.5e-100;
Conservative 0; Mismatches 166;
/mol_type="mRNA"
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Pooideae, Triticeae, Hordeum.
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Hordeum vulgare subsp. vulgare
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
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                B57 TIGCITCCATCITCCCAAGTICAGTGTAGGATCAATCAATGATGGAGACAATCACGTT
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/clone lib="K. Sato unpublished cDNA library,
Akashinriki vegetative stage leaves"
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Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)
Contact: Tadasu Shin-i
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|mol_type="maNNA"
|cultivar="Akashinriki"
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/db_xref="taxon:112509"
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                  Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Hordeum.
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/clone_lib="K. Sato unpublished cDNA library, cv.
Akashinriki vegetative stage leaves"
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Pred. No. 2.5e-99;
0; Mismatches 143; Indels 21
                                                                                             1 (bases 1 to 686)
Sato,K., Saisho,D. and Takeda,K.
Barley BST sequencing project in NIG and Okayama Univ Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                             organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                                                                   1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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/db_xref="taxon:112509"
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  Hordeum vulgare subsp. vulgare
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Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooldeae, Triticeae, Hordeum.
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Akashinriki vegetative stage leaves"
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Pred. No. 3e-98;
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
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Barley EST sequencing project in NIG and
Unpublished (2002)
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/sub_species="vulgare"
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Location/Qualifiers
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ISM Hordeum vulgare subsp. vulgare
ENtaryorda; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Entaryorda; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

SE (bases 1 to 693)

Sato,K., Saisho,D. and Takeda,K.

Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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Email: tshini@genes.nig.ac.jp.
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Vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
baak28d17 3', mRNA sequence.
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                                                                         CGCTATTTGGATCTCTCGGGTAATTCATTGGTTGGGGAGGTACCAAAAAGTTTGCAGATA
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                                                                       /sub_species="vulgare"
|db_xref="texaon:112509"
|/clone="baak28d17"
|/tissue_type="leaves"
|dev_stage="vegetative stage"
|dev_stage="vegetative stage"
|Akashinriki vegetative stage leaves"
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BJ461908 K. Sato unpublished cDNA library, cv. Akashinriki BJ461908 K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baak21401 3', mRNA sequence.

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GI:21140417
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Best Local Similarity 75.3%;
Matches 503; Conservative
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/sub_species="vulgare"
/db_xref="taxon:112509"
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Location/Qualifiers
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/mol type="mRNA"
/cultiva="Chinaee Spring"
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/dev stage="Five-day old seedling"
/dev stage="Five-day old seedling"
/dev stage="Five-day old seedling"
/lab_nost="E. col: Solk"
/lab_nost="E. col: Solk"
/loce="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised to give plluescript phagemids in the TV close lab (Choi, Close, Fenton) at the University of California, Riverside: Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                               BE490074 588 bp mRNA linear EST 31-JUL-2000 WHE0365_G07_N13ZS Wheat cold-stressed seedling cDNA library Iriticum aestivum cDNA clone WHE0365_G07_N13, mRNA sequence.
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US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticum.

1 (basea: Triticaea; Triticum.

1 (basea: Lo S88)

Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.

The structure and function of the expressed portion of the wheat genomes - Cold-stressed seedling cDNA library
Unpublished (2000)
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                        86 GCTCACCTTGTTGTCCCGAGTTCGGTGTAGCTCACAATCACTGGTGGGGCCCAATCGTGTT
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Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
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AGCAACAAGTCGTAACAGATGGTTAATAT---
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Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Hordeum:

1 (Dasses 1 to 632)

Sato, K., Saisho, D. and Takeda K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadasu Shin-i

Contact: Ta
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                                          20 CGGCTAGAGGAGCTCAACCTTGCCAACAACAAAACTGGTCGGTACCATCCCATCGTGGATT
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/organism="Hordeum vulgare subsp. vulgare"
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36.7%;
al Similarity 76.7%;
467; Conservative
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Pooidaea; Triticae; Hordeum.
1 (bases 1 to 671)
Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Okayama Univ
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/clone="baak42e04"
/tissue_type="leaves"
/dev_stage=vegetative_stage"
/clone_lib="K. Saco unpublished cDNA library,
Akashimriki vegetative stage_leaves"
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Pred. No. 6e-97;
0; Mismatches 133;
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nilarity 77.1%;
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/db_xref="taxon:112509"

/clone="baak46n01"

/tissue_leaves"

/dw stage="vegetative stage"

/clone_lib="K. Sato unpublished cDNA library,

Akashinriki vegetative stage leaves"
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Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 359.4; DB 4;
Pred. No. 4.2e-96;
0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/cultivar="Akashinriki"
          JOURNAL
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bJ450137 K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baaks28417 5', mRNA sequence.
                                                                       Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticae; Hordeum.
1 (bases 1 to 609)
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                       ATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATAT
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Contact: Tadaus Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6856 Fax: 15-559-81-6856 Fax: 15-559-81-685
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/clone_lib="K. Sato unpublished cDNA library,
Akashinriki vegetative stage leaves"
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/mol_type="mRNA"
/cultivar="Akashinriki"
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/db_xref="taxon:112509"
/clone="baak28d17"
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BJ462238 K. Sato unpublished cDNA library, cv. Akashinriki
BJ462238 X. Sato unpublished cDNA library, cv. Akashinriki
BJ462238 X. mRNA sequence.
BJ462238 G. mRNA sequence.
BJ462238.1 GI:21140745
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Hordeum vulgare subsp. vulgare
Eukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACTGTCATATCCGGGAACAACAACAATGTGGCTGGGAAGAACAACAACTATCGTAACCGG 323
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/db_xref="taxon:112509"
/clone="baak24g16"
/tissue_type="leaves"
/dw stage="vegetative stage"
/clone_lib="K. Sato unpublished cDNA library,
Akashimriki vegetative stage leaves"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
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mol_type="mRNA"
/cultivar="Akashinriki"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contect: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Wishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tal: 5105595773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    632 ACTGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCATATTGTTACTGATAACAAT 691
324 ACCGTAACTGGTAGCAACCATGTCGTATCTGGGACAAACATATCGTAACTGACAACAAC 265
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticae; Triticum.

(bases 1 to 692)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D.,
Han, P.S., Hais, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
The structure and function of the expressed portion of the wheat
                                                                                                                                                                                           512 AACAATAGTGTTGGATCAGGGAACAACAATGTTGTTTCCGGGAATGACAACACGGTCGTA 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 AATGCCGTATCCGGGAATGACAATAATGTATCTGGGAGTTTCCATACCGTATCCGGAAGC 205
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                                                             511
                                                                                                                                                                                                                                                                                                                          572 TCTGGGAATAACAACCATGTGTCTGGGAGCAACAACACTGTTGTAACTGGAAGTGACAAT 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          692 AATGTTGTATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATACTGTATCAGGGGAG 751
564 CGGCTCAAGGGCTTCGCCATCGCTGGTCGTTCATCAGGTATGATTTTTACTAACATGCCA 505
                                                                                                   WHE0840 DOI H022S Wheat vernalized crown cDNA library Triticum aestivum cDNA clone WHE0840 DOI H02, mRNA sequence.
                                                                455 TTGCATGT---GAGCAGTAGAAGGACGCTCGATGAAGAACCAAATACAATATAGGGACC
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/cultivar="Chinese Spring"
/cultivar="Chinese Spring"
/clone="WHE0840 D01 H02"
/tissue_type="Crown tissue of seedling"
/dev stage="Five-week old seedling"
/dev stage=
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Sequence have been trimmed to remove vector sequence and low
quality sequence with pitmed score less than 20
Seq primer: Straagene SK primer.
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Unpublished (2000)
Contact: Olin Anderson
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Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Hordeum.

E 1 (bases 1 to 689)

S Sato, K., Saisho, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadasus Shin-i

Contact: Tadasus Shin-i

Contact: Tadasus Shin-i

Contact: Tagasus Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers
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                       rcceggaacaacaargregcreggaecaacaacarcrarceraaceeggaacgacaar 385
                                                                                                                                                                                                                          AATGTTGTATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATACTGTATCAGGGGAG 751
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                                                                                            ACTGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCATATTGTTACTGATAACAAT 691
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|mol_type="mRNA"
|cultivar="Akashinriki"
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Matches 451, Conservative
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Site_1: EcoRI; Site_2: XhoI; Seeds were germinated and grown at 4 C for 5 weeks. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TV Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the op Anderson lab (all other authors).
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                                     500207009_A SC02_AAFC_ECORC_cold_stressed_winter_rye_seedlings
Scale cereale cDNA clone Sc02_07e09, mRNA sequence.
BE705098.1 GI:10093363
RESULT 15
BE705098/c
LOCUS
DEFINITION
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GGTTAATAT 841

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/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI; Site_2: Xho I; Sampled three-leaf seedlings treated for one week at 2oC, 12 hrs light/day. Library made with Stratagene UNIZAP XR Kit/(not packaged). cDNA is directly ligated into SK+/XhoI-EcoRI, then electroporated into TOPIO cells (Invitrogen)."
                                                                                                                                                                                                                                                 /mol_type="mRNA"

/cultivar="Puma (winter rye)"

/db_xref="taxon:4550"

/clone="Scv2 O'ee9"

/tissue type="leaf, crown"

/dev_stage="seedling three-leaf stage"

/clone_lib="Sc02_AAFC_ECORC_cold_stressed_winter_rye_seedl
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                                                                      Ontario,
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                                                                      Ottawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
Contact: Singh,J.A.
Bastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm,
OCG, Canada
TTel: (613) 759-1662
Fax: (613) 759-1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.5%; Score 348.2; DB 2; 75.5%; Pred. No. 9.8e-93; ative 0; Mismatches 143;
                                                                                                                                                                                                                            organism="Secale cereale"
                                                                                                                                                          Bmail: singhja@agr.gc.ca.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 460; Conservative
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74 GAATGATTT 66

Search completed: May 11, 2005, 01:33:58 Job time : 3917 secs

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6, Appli
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                                                                                                       May 11, 2005, 00:03:23 ; Search time 217 Seconds (without alignments) 7389.637 Million cell updates/sec
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Sequence 17, A
Sequence 34, A
Sequence 34, A
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Sequence 34, A
Sequence 19, A
Sequence 19, A
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Sequence 2
Sequence 2
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Sequence 4
Sequence 1
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-23-463-14
US-10-101-464A-212
US-10-101-464A-221
US-09-33-447A-6
US-09-34-267B-6
US-09-249-180-1
US-09-434-28B-12
US-10-101-464A-865
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US-10-101-464A-865
US-10-101-464A-865
US-10-101-464A-895
US-10-101-464A-897
US-09-228-96-39
US-10-101-464A-837
US-09-24B-976-15639
US-10-101-464A-837
US-09-24B-976-15639
US-09-24B-976-15639
US-10-101-464A-837
US-09-265-556-171
US-09-056-556-171
US-09-056-556-171
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%.
Maximum Match 100%
Listing first 45 summaries
                                                                         OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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980
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                                                                                                                                                                                                    Perfect score:
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GENERAL INFORMATION:

APPLICANT: Strabala, Timothy
APPLICANT: Mieuwenhuizen, Nicolaas
APPLICANT: Mieuwenhuizen, Nicolaen M.

TITLE OF INVENTION: Compositions Isolated from Plant Cell Signaling
FILE REFERENCE: 11000.1020.2

CURRENT APPLICATION NUMBER: 09/704,302

PRIOR APPLICATION NUMBER: 09/704,302

PRIOR APPLICATION NUMBER: 09/228,986

PRIOR PLIJNG DATE: 1999-01-10

PRIOR APPLICATION NUMBER: 60/162,866
                                                            694 TGTTGTATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATACTGTATCAGGGGAGCA 753
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                                                                                                                                              754 CAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATATCGTATCTGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 212, Application US/10101464A
Patent No. 6768041
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Best Local Similarity 63.9%;
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Strabala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-101-464A-212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-101-464A-212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   514 CAATAGTGTTGGATCAGGGAGCAACAATGTTGTTTCCGGGAATGACAACACGGTCGTATC 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    574 TGGGAATAACAACCATGTGTCTGGGAGCAACAACACTGTTGTAACTGGAAGTGACAATAC 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        634 TGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCATATTGTTACTGATAACAATAA 693
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4.6%; Score 44.8; DB 1; Length 7218;
Best Local Similarity 4.7%; Pred. No. 0.0033;
Matches 19; Conservative 216; Mismatches 173; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                    APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
ATTONNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                    Sequence 14, Application US/08232463
Patent No. 5670367
243 TCGGCGGCCCTTCCC 258
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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STRANDEDNESS: single
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; CLONE: pTZgpt-F1s
US-08-232-463-14
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                                                                                                                                                                       US-08-232-463-14/c
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APPLICANT: Lund, Adrian A
APPLICANT: Lund, Adrian A
APPLICANT: Bhattramakki, Dinakar
APPLICANT: Rhoads, David M.
TILLE OF INVENTION: Isolation and Characterization of Heat Shock Protein
FILE REFERENCE: UNNN52819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 504 CAGGGACCAACAATAGTGTTGGATCAGGGAGCAACAATGTTGTTTCCGGGAATGACAACA
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APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/952,267B
FILE APPLICATION NUMBER: US/09/336,447
PRIOR APPLICATION NUMBER: US/09/336,447
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
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CURRENT FILING DATE: 1999-02-12
EARLIER APPLICATION NUMBER: 60/076/014
EARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Created in Patentin Ver. 2.0, Edited in WordPerfect 6.1
SEQ ID NO 1
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4.1%; Score 40.4; DB 4; Length 3381;
Best Local Similarity 46.5%; Pred. No. 0.054;
Matches 131; Conservative 0; Mismatches 151; Indels 0
         1021 TCGGCTCTAATAATACCATTGACAGTGGCAAACAAAATGTCT 1062
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                                                                                                                                                   Sequence 6, Application US/09952267B Patent No. 6753417
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; Sequence 1, Application US/09249180
Patent No. 626848
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                          APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 3381
                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                             JS-09-952-267B-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 CGTCGTGGCGTTGCGGCTCCCCAAGCGCGCGTTGGAGGGATCATCCCCATCGTCGATTGG 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 gaggcrcaaggcrcaccgarrragaccrcgccrrcaacracrragagggccccaracc
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APPLICANT: AEBI, CHRISTOPH
APPLICANT: OCDE, LESLIE D.
APPLICANT: MACIVER, LSCLIE D.
APPLICANT: MACIVER, LSCBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT PILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIN VET. 2.1
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4.1%; Score 40.4; DB 3; Length 3381;
Best Local Similarity 46.5%; Pred. No. 0.054;
Matches 131; Conservative 0; Mismatches 151; Indels 0
                                                                                                                                                                                                                                                                                                                                     Query Match
4.1%; Score 40.4; DB 4; Length 396;
Best Local Similarity 58.2%; Pred. No. 0.013;
Matches 71; Conservative 0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         744 CAGGGGGGCACATACCGTATCCGGGAGCAACAATACTGTAT 785
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 221
LENGTH: 396
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Patent No. 6310190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-101-464A-221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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US-09-336-447A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 GAGGGGCCTCGCTGAGAACCTAAGCGGCAAAGGAGCCGTCCGCCTCCGCGCCGCATGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38.8; DB 3;
Pred. No. 0.11;
0; Mismatches 97;
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PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 840
                                             FILE REFERENCE: 30062-20030.00
CURRENT APPLICATION NUMBER: US/09/434,288
CURRENT FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 60/107,093
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
               CONSTRUCTS THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 840, Application US/10101464A
Patent No. 6768041
                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Streptomyces narbonensis
US-09-434-288-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%;
Matches 97; Conservative 0
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US-10-101-464A-840
               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-101-464A-840
                                                                                                                                                                                                                                                                                                                                             LENGTH: 1476
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Patent No. 6303767;
GENERAL INFORMATION:
APPLICANT: Betlach C., Melanie
APPLICANT: McDaniel, Robert
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
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AUTHORS: Blthon, Thomas E.
TITLE: Heat-Stress Response of Maize Mitochondria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)..(1028)
OTHER INFORMATION: Zea Mays L., Line B73
                                                                                                                                                                                                                                                                                                                                 LOCATION: (424)..(693)
OTHER INFORMATION: Heat Shock Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 52.5
Matches 85; Conservative
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LOCATION: (79)..(213)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(78)
PUBLICATION INFORMATION:
AUTHORS: Lund, Adrian A.
AUTHORS: Blum, Paul H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Poly A site
LOCATION: (1028) .. (1028)
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LOCATION: (736)..(1028)
                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                       CDS
(79)...(735)
                                                                                                                                                                                                            (1)..(1028)
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Zea mays
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PAGES: 1097-1110
DATE: 1998-03-00
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GENERAL INPORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwerhulzan, Micolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
FILE PEPLICATION NUMBER: 09/704,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1723 GCTTTCCTACAACGCACTTGAAGGTCTGATACCAGCTTCAATCAGTGAGCTTCAAAATCT 1782
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Best Local Similarity 56.2%; Pred. No. 0.16;
Matches 73; Conservative 0; Mismatches 57;
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GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Neuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TITLE OF INVENTION: 00000011020
CURRENT PRINCESTION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SEQ ID NO 39
LENGTH: 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 ACCACGACGACCTCCACGCGTTGAGGGGCCTCGCTGAGAACCTAAGCGGCAAAGGAGCCG 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.9%; Score 38.2; DB 3; Length 454; Best Local Similarity 51.5%; Pred. No. 0.077; Matches 88; Conservative 0; Mismatches 83; Indels
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FASISEQ for Windows Version 4.0
SOFTWARE: FASISEQ for Windows Version 4.0
SEMETH: 2735
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Patent No. 6359198
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; ORGANISM: Eucalyptus grandis
US-10-101-464A-865
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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Nicolaas
APPLICANT: Higgins, Collean M.
TILL OF INVENTION: Compositions Isolated from Plant Cells
TILLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REPERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-11-01
PRIOR PILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
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Patent No. 6768041

GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling; FILE REFERENCE: 11000.1020c2
1783 TCAGGACATGGATTTCTCCTCCAACAAATTGTCAGACTTGGACTTCGAAGCTTTGATATT 1842
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                   Sequence 268, Application US/10101464A, Patent No. 6768041; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 TGGTTGGGGAGGTACC 378
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ORGANISM: Eucalyptus grandis
                                                                                                                                               1843 rccerrcare 1852
                                                                                         394 ACGCCTCAAG 403
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US-10-101-464A-865
                                                                                                                                                                                                                                   RESULT 10
US-10-101-464A-268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 CCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTATTTGGATCTCTCGGGTAATTCATT 363
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                                                                                                                                                                                                                                                Score 38.2; DB 4; Length 498;
Pred. No. 0.081;
0; Mismatches 83; Indels
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobett, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PILLING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15539
LENGTH: 505
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                              NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 421
LENGTH: 498
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        PRIOR FILING DATE: 2000-01-11
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Best Local Similarity 51.5
Matches 88; Conservative
                                                                                                                                       TYPE: DNA
ORGANISM: Pinus radiata
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## APPLICANT: ACOUSTION:
## APPLICANT: ACOUSTION:
## APPLICANT: Higgins, Colleen M.
## APPLICANT: Higgins, Colleen M.
## TITLE OF INVENTION: Compositions Isolated from Plant Cells
## TITLE OF INVENTION: Their Use in the Modification of Plant Cell Signaling
## TITLE OF INVENTION: Their Use in the Modification of Plant Cell Signaling
## TITLE OF INVENTION: Their Use in the Modification of Plant Cell Signaling
## TITLE OF INVENTION: Their Use in the Modification of Plant Cell Signaling
## TITLE OF INVENTION OF ACOUSTION:
## TITLE OF INVENTION NUMBER: 09/20,302
## PRIOR PILING DATE: 1999-01-12
## PRIOR PILING DATE: 1999-01-12
## PRIOR PILING DATE: 1999-11-01
## PRIOR PILING DATE: 1999-11-01
## PRIOR PILING DATE: 2000-01-11
## PRIOR FILING DATE: 2000-01-11
## NUMBER OF SEQ ID NOS: 989
## SOFTWARE: FastSEQ for Windows Version 4.0
## SEQ ID NOS: 989
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APPLICANT: Strabala, Timothy
APPLICANT: Miscuenthuizen, Nicolaas
APPLICANT: Miscuenthuizen, Nicolaas
APPLICANT: Miscuenthuizen, Nicolaen
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.102602
CURRENT APPLICATION NUMBER: 09/104,302
FRIOR APPLICATION NUMBER: 09/28,966
FRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01

FRIOR APPLICATION NUMBER: 60/162,866

PRIOR FILING DATE: 1999-11-01
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; Sequence 421, Application US/10101464A
; Patent No. 6768041
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Patent No. 6768041
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Matches 88; Conservative
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ORGANISM: Pinus radiata
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Search completed: May 11, 2005, 02:55:00 Job time : 221 secs

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Abq77273 Oligonucl
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Aaa79412 Eucalyptu
Aav41343 M. catarr
Aa19322 Human exc
Aa19327 Human exc
Aa193672 Human exc
Aa61931 DNA encod
Adm80069 Spiramyci
Adm97585 a ambofac
Adm97585 a sambofac
Adm97581 anbofac
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Ab118481 Drosophil
Adm03281 Human cDN
Ab118481 Drosophil

Abz23668 H. pylori Abl17081 Drosophil Abl17080 Drosophil Aaa50251 Maize hea

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New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
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601 CAACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTATC 660
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                                                                                                                     GTCTGGAAGCTTCCATACTGTATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATAC
                                                                                                                                                                                              TGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACAGATGGTTAATA
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                                                                                                                                                                                                                                                                                                                                                  New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fescue; cold tolerance; transgenic; plant; antigout;
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/product= "Antifreeze protein"
/transl_except= (pos:410. .412,aa:Xaa)
/note= "Xaa= unknown"
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41. .850
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(WRIG-) WRIGHTSON SEEDS LTD.
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113. .847
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                                                                   The present sequence is that of cDNA encoding AFP2, an antifreeze protein of perennial ryegrass. The cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall feacue) antifreeze proteins and the polymucleotides cryegrass and tall feacue) antifreeze proteins and the polymucleotides encoding them ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thoreby inhibiting expression of an antifreeze polypeptide. The crissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology creagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 980 BP; 264 A; 223 C; 253 G; 240 T; 0 U; 0 Other;
                                     Claim 1; SEQ ID NO 3; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        980; Conservative
biocrystals (e.g. gout)
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Best Local Similarity
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33. .121
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(WRIG-) WRIGHTSON SEEDS LTD
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                             The present sequence is that of cDNA encoding an antifreeze protein of tall fescue. The cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41458-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kindey stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
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Pred. No. 5.2e-273;
0; Mismatches 31; Indels
Claim 1; SEQ ID NO 4; 71pp; English
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Best Local Similarity 96.2%;
Matches 949; Conservative
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Sequence 1006 BP; 248 A; 261 C; 260 G; 237 T; 0 U; 0 Other;

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                                                                  Gaps
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      DB 12; Length 1006;
Score 541.6; DB 12; Length
Pred. No. 5.3e-159;
0; Mismatches 194; Indels
55.3%;
llarity 76.5%;
Conservative
Query Match
Best Local Similarity
Matches 756; Conserv
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                          TACTGTATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAA
                                              TACCGTATCCGGGGGGCACAATACCGTCTCTGGGAGCAACAATACCGTATCTGGGAGCAA
                                                                             CCATATCGTATCTGGGAGCAACAAGTCGTAACAGATGGTTAATATTCTGTAGGTGCAGG
                                                                                                                                                                                    TAGATGGAGACAATCACGTTATGTAACTTCA-GGATATGGCATACTTTTC---CTTTAAA
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P-PSDB; ADM41480.
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The present sequence is that of cDNA encoding, an antifreeze protein of perennial ryegrass. The cDNA was isolated from a leaf and pseudostem cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifrese proteins and the polynucleotides encoding them ADM41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from
                                                                                                                                                                                                                                                                                                                                                                                                                                             911 TCACAGTCAGTTGGTGCGTTCAATCGCGTTAATGTAACTTCATGGATATACCATACTTTTC
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                                                                                                                CCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACAGATGGTTAATATTCTG
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ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41458-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1008 BP; 256 A; 265 C; 251 G; 236 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.7e-147;
0; Mismatches 194; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protect a plant from damage due to frost or freezing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.4%; Score 503.6; DB 12; 74.3%; Pred. No. 4.7e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 74.3 nes 742; Conservative
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CTGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAGTCGTAACAGATGGTTAAT

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different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to frost or freezing.
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Sequence 1007 BP; 252 A; 265 C; 253 G; 237 T; 0 U; 0 Other;

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122 242 446 ACCACGACGACCTCCACGCGTTGAGGGGCCTCGCTGAGAACCTAAGCGGCAAAGGAGCCG 182 AAACAGCAAGCGGCCGCGTCGTGGCGTTGCGGCTCCCCAAGCGCGCCCTTGGAGGGATCA 302 396 479 483 599 603 629 663 CAGGGACAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAATG 719 723 783 TGGTTGGGGAGGTACCAAAAAGTTTGCAGATACGGCTCAAGAGCCTCACCACTGACAGCC 422 ATTGAATCCATCTATAGCATAGCACTGCTGAATCCATGGCGAAATGCTTGATGCTTC 96 AATCAAGGTTTCTTGTTCAATCCATGCCTGAATACATGGCAAAGTGTTGCATGCTGCTGG TCTTCTTGGGGTTCATCTTGCAGGTGGCAGGA-----GCAACGTCGTGGTCGTGCC TCCGCCTCCGCGCGCATGGTCCGGCGCCTCATGCTGCAGCTGGGAAGGTGTGGGATGCG | | ACGTGCCAGCGGCCGTGTCACGGCTTTGTGTGTTCCCCAGGAGCGGCCTCCACGGGGCCAA TCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTATTTGGATCTCTCGGGTAATTCAT TCCGGTCATGGATTTTTCAGCTTCACCACCCTACGCTACGCATTGTTTCAGGTAATGCAT TGGTTGGCGAGGTACCCAAGAATCTGCAGGTACAGCTCAAAGGCATCACC------AGTCACTCGGTATGGGTTCCATTAACATGCTATTGCATGTGA---GCAGTAGAAGAACGC ------AACATGCCATTGCATGTGATGCGTAACAGAAGATCAC TCGATGAAGAACCAAATACAATATCAGGGACCAACAATAGTGTTGGATCAGGGAGCAACA 484 TCGACGAGCAGCCCAATACAATTTCTGGGAGCAACAATACTGTCAGATCCGGGAGCAAAA ATGTTGTTTCCGGGAATGACAACACGGTCGTATCTGGGAATAACAACCATGTGTCTGGGA GCAACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTAT GCAACAACACTGTCGTAAGTGGGAATGACAATACCGTAACCGGCAGCAACCATGTCGTAT CAGGGACAAACCATATCGTTACAGACAACAATAACGTATCCGGGAACGATAATAGTG Gaps 68; DB 12; Length 1007; 50.3%; Score 492.8; DB 12; Length ilarity 73.6%; Pred. No. 1.2e-143; Conservative 0; Mismatches 197; Indels Local Similarity 739; 337 12 37 72 97 157 183 217 243 277 363 397 423 447 480 540 544 909 099 664 720 123 303 Query Match 604 Matches g 셤 g g g g g 요 g g

tall fescue. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41458-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold archean enganism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the

present sequence is that of cDNA encoding an antifreeze protein of

903 843 880 939 784 CCGTATCTGGGAGCAACCACGTTGTATCTGGAAGCAACAAAGTCGTGACAGACGCTTAAT TGTAGCTTACAATCAATAGATGGAGACAATCACGTTATGTAACTTCA-GGATATGGCATA New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted fescue, cold tolerance, transgenic, plant, antigout, nephrotropic, cytostatic, gene, ss. CITITICCIACIAIAIAAAITIICCCITIACAIAAAAAAA 1007 CTTTTC---CTTTAAATAAAGCTTCCCTTTACATAAAAAAA 980 "Antifreeze protein" 840 ATTCTGTAGGTGCAGGATTGCTTCCATCTT Fish SA; Location/Qualifiers 76. .909 /*tag= b /product= "Antifreeze Claim 1; SEQ ID NO 6; 71pp; English. antifreeze protein cDNA. DEV CORP LTD BP ú ADM41463 standard; cDNA; 1230 09-SEP-2002; 2002US-0409557P. 09-SEP-2003; 2003WO-NZ000199 Hall 76. .141 /*tag= a 142. .906 /*tag= c (first entry) Schedonorus arundinaceus. GENESIS RES & DE WRIGHTSON SEEDS (e.g. gout) Demmer J, Shenk MA, WPI; 2004-248453/23 P-PSDB; ADM41476. WO2004022700-A2 biocrystals 03-JUN-2004 Tall fescue Antifreeze; litholytic; sig_peptide 18-MAR-2004 mat_peptide ADM41463; 881 940 964 (GENE-) ADMA1463
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ADM41464
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genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreze polypetide. The antifreze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
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                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                 Length 1230;
                                                                                                                                                                                                                                                                                      78;
                                                                                                                                                                                                            Sequence 1230 BP; 327 A; 279 C; 298 G; 326 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                    0; Mismatches 198; Indels
                                                                                                                                                                                                                                               Score 451.2; DB 12;
Pred. No. 1.5e-130;
                                                                                                                                                                                                                                                                                                                           33 CCATGCCTGAATACATGGCAAAGTGTTGCATGCTGCTGGT
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.0%;
Matches 708; Conservative
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                                 893 TGACAGGAGATGAATGATTTGTCAGGGGATCGTTTCCATCTTCCCTAAAGGAGCACTCAC
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a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to frost or freezing.
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llarity 71.2%; Pred. No. 3.7e-128;
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The present sequence is that of cDNA encoding an antifreeze protein of tall fescue. The cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41488-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a forzer food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocryetals associated with disorders such as gout and kidney stones, to preserve the
                866 TCTTCCCAAGTTCAGTGTAGCTTACAATCAATAGATGGAGACAATCACGTTATGTAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antifreeze proteins and encoding polymucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                          fescue; cold tolerance; transgenic; plant; antigout; nephrotropic; cytostatic; gene; ss.
                                                                                           carggararaccartriccraracrita 1027
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                                                                                                                                                                                                                                                                             antifreeze protein cDNA
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P-PSDB; ADM41479.
                                                                                                                                                                              ADM41466 standard;
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957 ACTIGACAGAGITICAGIGIAGCACTCAATCACTIGGIGGGGGACAAICGGGITATGIAACT 1016
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viability of a molecular biology reagent, to destroy unwanted tissue in patient e.g. tumour tissue, and to protect a plant from damage due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 GACTGGTCGGCACCATCCCATCGTGAGCTTGACCACCTTCTCTCTTGGATC
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                                                                                                     Score 421.8; DB 12; Length 1246;
Pred. No. 2.7e-121;
0; Mismatches 192; Indels 103;
                                                                      Sequence 1246 BP; 313 A; 294 C; 307 G; 332 T; 0 U; 0 Other;
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                                                                                                         43.0%;
                                                                                                                     Best Local Similarity 70.1%;
Matches 690; Conservative
                                   frost or freezing
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New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                       Antifreeze, perennial ryegrass; cold tolerance; transgenic; plant; antigout; litholytic; nephrotropic; cytostatic; gene; ss.
                                                                                                                                                                                         "Antifreeze protein"
                                                                                                       Perennial ryegrass antifreeze protein cDNA.
              1017 rcargedarararcaraccrrrccr 1041
                                                                                                                                                                                                                                                                                                                                   SA;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 13; 71pp; English
                                                                                                                                                                                                                                                                                                                                  Fish
                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                          GENESIS RES & DEV CORP LTD
                                                        ВЪ.
                                                        ADM41470 standard; cDNA; 1083
                                                                                                                                                                                                                                                                                                                                  Hall C,
                                                                                                                                                                                                                                                                         09-SEP-2003; 2003WO-NZ000199
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                                                                                                                                                                                                                                                                                                                                  Demmer J, Shenk MA,
                                                                                                                                                                                                                                                                                                                                                  2004-248453/23.
                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ADM41483
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                                                                                                                                                 Lolium perenne
                                                                                        03-JUN-2004
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The present sequence is that of cDNA encoding, an antifreeze protein of perennial ryegrass. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them ADMA1458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the calls of the organism, thereby inhibiting expression of an antifreeze polypeptide. The cryopreservation of a call or tissue, as a food additive of a freze from product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to frost or freezing.

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ADM41462 standard; cDNA; 1084
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ADM41462
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                                                                                                                                                           CCAGAAACTTAAATCCATGGCGAAAATGTTGGCTGCTGCTGCTCTTCTTGGTTCCTCTTGC
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                                                                                            Gaps
                                                                                        90;
                                                Length 1083;
290 A; 257 C; 262 G; 274 T; 0 U; 0 Other;
                                                                                        Indels
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                                            Score 419; DB 12;
Pred. No. 1.9e-120;
0; Mismatches 205;
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                                         42.8%;
al Similarity 70.4%;
702; Conservative
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  Sequence 1083 BP;
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                                         Query Match
Best Local
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The present sequence is that of cDNA encoding AFP3, an antifreeze protein of perennial ryegrass. The cDNA was isolated from a root cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them can different times of year (winter and spring) and from different parts of the plants. The polymucleotides were isolated from tissues taken to the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, carchaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding cyponeme of the organism, or introducing double-stranded RNA corresponding expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a viability of a molecular biology reagent, to destroy unwanted tissue in a content of the collection of a collection of a collection of an antifreeze protein can be used to the described by biocrystals New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted Antifreeze, perennial ryegrass, cold tolerance; transgenic; plant; antigout; litholytic; nephrotropic; cytostatic; gene; ss. "Antifreeze protein AFP3" to protect a plant protein AFP3 cDNA Fish SA; Location/Qualifiers 60. .905 Claim 1; SEQ ID NO 5; 71pp; English. Ęij. and GENESIS RES & DEV CORP WRIGHTSON SEEDS LTD. Perennial ryegrass antifreeze ΰ 09-SEP-2002; 2002US-0409557P. 09-SEP-2003.; 2003WO-NZ000199 tissue, Hall /*tag= b /product= /*tag= a 118. .902 /*tag= c (first entry) 60. .117 biocrystals (e.g. gout) Demmer J, Shenk MA, WPI; 2004-248453/23. P-PSDB; ADM41475. tumour WO2004022700-A2 Lolium perenne. 18-MAR-2004. 03-JUN-2004 sig_peptide mat_peptide patient (GENE-) (WRIG-) Key

Sequence 1084 BP; 290 A; 258 C; 262 G; 274 T; 0 U; 0 Other;

Query Match

Length 1084; 42.6%; Score 417.4; DB 12; BP.

standard; cDNA; 1064

ADM41465

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455
                                                                    CCAGAACTTAATCCATGGCGAAATGTTGGCTGCTGCTGCTCTTCTTGGTGTTTCCTCTTGC 105
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                                                                                                                                                                                                                                                                                                       GGCTCC------CCAAGCGCG 287
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                                                 CCATGCCTGAATACATGGCAAAGTGTTGCATGCTGCTGGTCTTTGGGGTTCATCTTGC
                     Gaps
                   90;
   Pred. No. 6e-120;
0; Mismatches 206; Indels
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   70.3%;
                  701; Conservative
Best Local Similarity
Matches 701; Conserv
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The present sequence is that of cDNA encoding AFP4, an antifreeze protein of perennial ryegrass. The cDNA was isolated from a leaf and pseudostem cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreze proteins and the polynucleotides encoding them ADMA1458-ADMA1483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promocer sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent. To decreasing the tissue in a patient e.g. tumour tissue, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                              Antifreeze, perennial ryegrass; cold tolerance; transgenic; plant; antigout; litholytic; nephrotropic; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 40.2%; Score 394.4; DB 12; Length 1064; Local Similarity 67.2%; Pred. No. 1e-112; Lonservative 0; Mismatches 226; Indels 121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1064 BP; 263 A; 274 C; 267 G; 260 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to protect a plant from damage due to frost or freezing
                                                                                                                                                                                                                                                                                               "Antifreeze protein AFP4"
                                                                                                            Perennial ryegrass antifreeze protein AFP4 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fish SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 8; 71pp; English.
                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-2003; 2003WO-NZ000199
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/product= '
55. .120
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121. .894
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The present sequence is that of cDNA encoding an antifreeze protein of tall fescue. The cDNA was isolated from a basal stem cDNA expression control interacts. The invention provides forage grass (peremital ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them fescue) antifreeze proteins and the polymucleotides encoding them at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold cold cold archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting cold a manificeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by blocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
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                                                                                                                                                                                                                                       fescue; cold tolerance; transgenic; plant; antigout; nephrotropic; cytostatic; gene; ss.
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0; Mismatches 116; Indels
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                                                                                                                                                                                 antifreeze protein cDNA.
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Best Local Similarity 74.8%;
Matches 353; Conservative 0
ADM41459 standard; cDNA; 959
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142. .810
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WRIGHTSON SEEDS
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                                                                                                                                                                                                                                       Antifreeze;
litholytic;
                                                                                                                     03-JUN-2004
                                                                                                                                                                              Tall fescue
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This sequence encodes the plant anti-freeze protein of the invention. The anti-freeze protein is characterised in that at least 40% of its amino acids are from the group of serine, threonine and asparagine. The anti-freeze protein can be used in frozen food products, especially frozen
                                                                                                        559
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                         292 AGTITCCAGATAITGCICAAAGGCTICACCACCGCTGGCGTTCACTGGGTAAGGCGTTC 351
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                                                                             352 ACTAACATGCCATTACATGTGAAGTCTAGCCAAGGAACACTCGACGAAGAACACAATACA 411
                                                                                                                        ATAACTGGGATCAATACTGTCAAATCCGGGAGCAACAATGTTGTTTCTGGGAACGAT 471
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                                                                                                                                                                                                                                                                                                                                                        711
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                                                                                                                                                                              472 AACACTGTCATATCCGGGAACAACGTCGTGTCCGGGAGCCACAACACGTCGTATTT
                                                                                                        ATATCAGGGACCAACAATAGTGTTGGATCAGGGAGCAACAATGTTGTTTCCGGGAATGAC
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AGTTTGCAGATACGGCTCAAGAGCCTCACTGACAGCCAGTCACTCGGTATGGGTTCC
                                                     ATTAACATGCTATTGCATGTGAGCAGTAG----AAGAACGCTCGATGAAGAACCAAATACA
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                                                                                                                                                                                                                                                                                                                                                                                                             New plant anti-freeze protein useful in frozen food products.
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P-PSDB; AAY22472.
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confectionery. Anti-freeze proteins are especially used in food products, which are heated, e.g. by pasteurisation, blanching or sterilisation or prior to freezing. Plants transformed with a nucleic acid sequence encoding the anti-freeze protein have an increased frost tolerance. Prior art anti-freeze proteins have not been applied to commercially available code food products, due to high costs and complicated processes for obtaining to the protein. Also prior art anti-freeze proteins have tended to destabilise during processing especially during the pasteurisation step. This is overcome by the present anti-freeze protein. The anti-freeze proteins provide an ice particle size following an ice recrystallisation inhibition assay of 15 mu M or less. The anti-freeze protein ingredient means that mixes can be frozen under quiescent conditions, e.g. in a shop or home freezer without the formation of unacceptable ice crystal shapes and hence with a texture different to products normally obtained via
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GATGAACAGCCGAATACGATTTCTGGGAGCAACAATACTGTCAGATCCGGGAGCAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                   482 GATGAAGAACCAAATACAATATCAGGGACCAACAATAGTGTTGGATCAGGGAGCAACAAT
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                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                             Length 357;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                         Sequence 357 BP; 116 A; 80 C; 89 G; 72 T; 0 U; 0 Other;
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55. .114
                                                                                                                                                                                                                                                                                                                                         Query Match 27.0%; Score 264.2; DB 2; Best Local Similarity 83.8%; Pred. No. 4.4e-72; Matches 299; Conservative 0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perennial ryegrass antifreeze protein AFP1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM41458 standard; cDNA; 841 BP
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/*tag= c
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26-SEP-2001; 2001US-0325277P.
26-SEP-2001; 2001US-0325448P.
04-APR-2002; 2002US-0370620P.
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                                                                                                                                                                                                                                                                                                                                                              06-MAY-2004 (first entry)
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Goff SA, Katagiri F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
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KATAGIRI F.
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PROVART N.
RICKE D.
ZHU T.
                                                                                                                                                                                                                                                                                                                                                                                                                      Plant cDNA #1496
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                                                                                                                                                                                                                                                                                                    ADJ40496;
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(RICK/)
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(BRIG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GOFF/)
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                                                                                                                                                                                                           ADJ40496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of cDNA encoding APP1, an antifreeze protein of perennial ryegrass. The cDNA was isolated from a pseudostem cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41458-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The plymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating on antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded NNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 AAAAGTTTGCAGATACGGCTCAAGAGCCTCACCACTGACAGCCAGTCACTCGGTATGGGT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCATTAACATGCTATTGCATGTGAGCAGTAG---AAGAACGCTCGATGAAGAACCAAAT 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAATATCAGGGACCAACAATAGTGTTGGATCAGGGAGCAACAATGTTGTTTCCGGGAAT 556
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                                                                                                                                                                                                                                                                                                                                                        reeze proteins and encoding polynucleotides, useful for ig cold tolerance in organisms, as food additives, or for tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACAACACGGTCGTATCTGGGAATAACAACCATGTGTCTGGGAGGAACAACACTGTTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 841 BP; 216 A; 217 C; 222 G; 186 T; 0 U; 0 Other;
                                                                                                                                                                                                              Fish SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1; 71pp; English.
                                                                                                                    GENESIS RES & DEV CORP
                                                                                                                                                                                                           Demmer J, Shenk MA, Hall C,
09-SEP-2003; 2003WO-NZ000199.
                                                          2002US-0409557P
                                                                                                                                                                                                                                                                                                                                                        New antifreeze proteins and modulating cold tolerance in
                                                                                                                                             (WRIG-) WRIGHTSON SEEDS LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                              biocrystals (e.g. gout).
                                                                                                                                                                                                                                                               2004-248453/23
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                                                                                                                                                                                                                                                                                              P-PSDB; ADM41471.
                                                       09-SEP-2002;
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                                                                                                                 (GENE-)
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Matches
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leaf-and/or stem., panicle, root- or pollen-specific or preferencial or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, eg. soybean, alfalfa, sumflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, sorghum, rice or wheat. The polynucleotides and the polypeptides they encode are useful for manipulating crop plants to alter or improve phenotypic characteristics, to produce large quantities of oil or proteins, to incur resistance to insecticides, viruses or fungi, and to
                                                         681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant, gene, 88; transcription; plant genome augmentation; cereal; soybean, alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet; maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; salt tolerance; cold tolerance; drought tolerance; plant nutrition; apical dominance; dwarfism; early flowering; antiviral; antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.
The invention relates to plant nucleotide sequences that direct seed-
                                                                                                                                        797 CATATCGTATCTGGGAGCAACAAAGTCGTAACAGATGGTTAATATTCTGTAGGTG
                                                                                                                                                                                                  <u>ن</u>
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rt N, Ricke D,
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Kreps J, Provart N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ40496 standard; cDNA; 4536
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incur stress tolerance (e.g. salt, cold or drought) to ensure the plants have a high nutritional value with reduced apical dominance or dwarfism, early flowering or alterned metabolic pathways. This sequence respresents a plant nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at sequata.uspto.gov/sequence.html.
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Sequence 4536 BP; 1102 A; 1247 C; 1221 G; 965 T; 0 U; 1 Other;

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	Gaps	CAGAGAG
4536;	6 ;	上してして
Length	Indels	しこうごうじゅうよ
Score 79.4; DB 12; Pred. No. 2.2e-13;); Mismatches 86;	104 GOAACGITCGIGGITCGICACCACCACGACGACCACGACGACGACGACGACGACGACG
8.1%;	ative	
Query Match 8.1%; Score 79.4; DB 12; Length 4536; Best Local Similarity 63.1%; Pred. No. 2.2e-13;	Matches 157; Conserva	Ov 104 GCAACGTCGTC

	135	220	195
	76 GCTGCGGCGCCCATGCCACCCGGAAGACCTCCTCGCGCTGCGGGCATTTGCGGGGGAAT 135	164 CTAAGCGCCAAAGGAGCCGTCCGCCTCCGCGCCGCATGGTCCGGCGCCTCATGCTGC 220	136 CTCTCTGCGGGTGGGGGCGCCGGACTCCGCGCCGCGTGGTGGTGGTGGTGGTGGTGGTGC 195
•	Ор	ć	Q Q

196 GCCTGGGACGCCTGCGACGCCGC -- CGCCCGAGTCACGGCGCTGCCCCC 252 221 AGCTGGGAAGGTGTGGGAAGCAAACAGCGGCCGCGTCGTCGTGGCGTTGCGGCTCCCCC 280

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281 AAGCGCGCCTTGGAGGCATCATCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTAT 340 ઠે 셤

341 TTGGATCTC 349

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313 crccaccrc 321

Search completed: May 11, 2005, 00:27:35 Job time : 657 secs

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Query Match
Best Local Similarity 63.1%;
Matches 157; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 77805, A Sequence 1496, Ap Sequence 4582, Ap Sequence 568, App Sequence 47843, A Sequence 102064, Sequence 102066, Sequence 102066, Sequence 102066, Sequence 102066,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 102065,
Sequence 102066,
                                                                                                                                                              May 11, 2005, 01:34:03 ; Search time 704 Seconds (without alignments) 8511.756 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NBW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_NBW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO7_NBW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_NBW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/USOP_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*
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17: /cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/USIOB_PUBCOMB.seq:*
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Compugen Ltd.
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US-10-260-238-568
US-10-1437-963-47843
US-10-027-633-102064
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US-10-260-238-1496
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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, William Cao, 
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Sequence 212, App
Sequence 212, App
Sequence 67222, A
                                                                      47358, A
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Sequence 105088,
Sequence 24982, A
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Sequence 3863, A
Sequence 3864, A
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US-10-437-963-79739

US-10-101-464-861

US-10-101-464-861

US-10-437-963-4738

US-10-087-192-1930

US-10-719-993-26

US-10-719-993-6767

US-10-719-993-6767

US-10-424-599-138064

US-10-424-599-138064

US-10-424-599-138064

US-10-425-115-3469

US-10-425-115-3469

US-10-425-115-3469

US-10-437-963-3963

US-10-363-3483-3863

US-10-363-3483-3863

US-10-363-4834-3863

US-10-363-4834-3864

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US-10-363-4834-3863

US-10-425-115-6722

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Pred. No. 2.2e-14;
0; Mismatches 86;
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OTHER INFORMATION: unsure at all n locations
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; Sequence 77805, Application US/10437963
; Publication No. US20040123343A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
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     ORGANISM: Oryza sativa
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: BROMOTERS FOR REGULATION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-4
PRIOR FILING DATE: 2001-09-6
PRIOR FILING DATE: 2001-09-6
SPRIOR FILING DATE: 2002-04
NUMBER OF SEQ ID NOS: 6077
LENGTH: 4536
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; OTHER INFORMATION: n = any nucleotide
US-10-260-238-1496
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Publication No. US20040016025A1
GENERAL INFORMATION:
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APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Glazebrook, Jane
APPLICANT: Katagiri, Fumiyaki
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Ricke, Darrell
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                                                                                                                                                                                                                                253 GGGCGAGGTCTCGAGGGGCCCATCCCGCCTCCTCGCCGCCCTCGCGGCCTCCAGGAC 312
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196 GCCTGGGACGGCGTCGCCTGCGACGCCGC---CGCCCGAGTCACGGCGCTGCGCCTCCCC 252
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APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Alche, Darrell
APPLICANT: Alche, Darrell
TITLE OF INVENTION: PROWOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REPERENCE: 60111-NP
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_11452C.1
US-10-437-963-4582
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Publication No. US20040016025A1
GENERAL INFORMATION:
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Goff, Stephen A.
Katagiri, Fumiyaki
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APPLICANT: Woughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
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204 CCGGCGCCTCATGCTGCAGCTGGGAAGGTGTGGGATGCGAAACAGCAAGCGGCCGCGTCG 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 CGGCCATCTCGCTGCAGGCCGCGGGGCTCTCCGGGACCCTCCCGGCGGATCGCCGGGC 271
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                         324 TIGAICACCTICGCIATITGGAICTCTCGGGIAATICATIGGIIGGGGAGGIACCAA 380
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APPLICANT: Wang, LOWIG G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR PLING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-22
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-09-28
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Publication No. US20020198371A1
GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(3221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-65-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 47843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 TCATCTTGCAGGTGGCAGGAGCAACGTCGTGGTCGTGCCACCACGACGACGACGTCTTCACGCGT 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 50.6; DB 17; Length
Pred. No. 5e-05;
0; Mismatches 154; Indels
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US-10-437-963-47843
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILLING DATE: 2002-09-26
FRIOR APPLICATION NUMBER: US 60/325,448
FRIOR PILING DATE: 2001-09-26
FRIOR PILING DATE: 2001-09-26
FRIOR PILING DATE: 2001-09-26
FRIOR PILING DATE: 2001-09-26
FRIOR PILING DATE: 2002-04-04
FRIOR PILING DATE: 2002-04-04
FRIOR PILING DATE: 2002-04-04
FRIOR PILING DATE: 2002-04-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.2%;
Best Local Similarity 48.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 143; Conservative
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; ORGANISM: Oryza sativa
US-10-260-238-568
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ORGANISM: Oryza sativa
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TYPE: DNA
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Best Local (
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108927.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/0/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-07-12
PRIOR PELING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/198,218
PRIOR APPLICATION NUMBER: US 60/195,389
PRIOR PILING DATE: 1099-101-28
PRIOR PILING DATE: 1999-101-28
PRIOR PILING DATE: 1999-102-8
PRIOR PILING DATE: 1999-00-28
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ITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITLE OP INVENTION: Identification and Mapping of Single Nucleotide
ITLE OP INVENTION: Identification and Mapping of Single Nucleotide
ITLE OP INVENTION: Identification in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/128,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR RILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
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                       Sequence 102065, Application US/10027632
Publication No. US20020198371A1
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Publication No. US20020198371A1
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Best Local Similarity 51.99
Matches 123; Conservative
.10-027-632-102065/c
                                                                                        GENERAL INFORMATION:
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ORGANISM: Human
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600 GCAACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTAT 659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          719 GTGTCTGGAAGCTTCCATACTGTATCAGGGAGCACAATACCGTATCCGGGAGCAACAAT 778
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE REPERSENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
FRIOR PILING DATE: 2002-04-30
FRIOR PILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-03-29
FRIOR PILING DATE: 2000-03-29
FRIOR PILING DATE: 2000-03-29
FRIOR APPLICATION NUMBER: US 60/185,218
FRIOR PILING DATE: 1999-112-3
FRIOR PILING DATE: 1999-11-3
FRIOR PILING DATE: 1999-11-3
FRIOR PILING DATE: 1999-10-30
FRIOR PILING DATE: 1099-10-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45.4; DB 13; Length 2498; Pred. No. 0.003; 1; Mismatches 112; Indels 1;
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Pred. No. 0.003;
1; Mismatches 112;
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FSELESC for Windows Version 4.0
SEQ ID NO 102066
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 102064
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Publication No. US20030204075A9
GENERAL INFORMATION:
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Best Local Similarity 51.94
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 51.9
Matches 123, Conservative
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                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
US-10-027-632-102066
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US-10-027-632-102064
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Publication No. US20030204075A9
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CAGGGA-CAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAAT 718
                                                                                                                                                                                           719 GTGTCTGGAAGCTTCCATACTGTATCAGGGAGCACAATACCGTATCCGGGAGCAACAAT 778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single Nucleotide
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TITLE OF INVENTION: Identification and Mapping of Single N
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108627.129
CURRENT PRILING DATE: 2002-04-30
CURRENT PILING DATE: 2002-04-30
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1090-10-24
PRIOR FILING DATE: 1090-10-24
PRIOR FILING DATE: 1090-10-24
PRIOR FILING DATE: 1099-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 102065
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Matches 123; Conservative
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RESULT 11 US-10-027-632-102066/c ; Sequence 102066, Application US/10027632

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Sequence 19739, Application US/10437963

Sequence 19739, Application US/10437963

Sequence 19739, Application US/10437963

Sequence 19739, Application US/10437963

Sequence 19739, Application No. US20040123343A1

APPLICANT: La Rovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Brazuk, Brad

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 30-21(5321)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 79739

LENGTH: 1614
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPRENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PLICATION NUMBER: US 60/218,006
PRIOR FLIING DATE: 2000-07-12
PRIOR FLIING DATE: 2000-07-20
PRIOR PLIING DATE: 2000-04-20
PRIOR PLIING DATE: 2000-03-29
PRIOR PLIING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR PLIING DATE: 1999-11-23
PRIOR PLIING DATE: 1999-08-09
PRIOR PLING DATE: 1999-08-09
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Best Local Similarity 51.9%;
Matches 123; Conservative
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US-10-027-632-102066
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Sequence 861, Application US/1010164A

Sequence 861, Application US/2030046728A1

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Nicolaas

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

FILE REPERENCE: 1100.1026.2

CURRENT APPLICATION NUMBER: 09/704,302

PRIOR FILING DATE: 2002-01-10

PRIOR PLING DATE: 1999-11-01

PRIOR PPLICATION NUMBER: 60/162,866

PRIOR PLING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: 60/162,866

PRIOR PLING DATE: 2000-01-11

**PRIOR APPLICATION NUMBER: 1999-11-01

**PRIOR PLING DATE: 2000-01-11

**NUMBER OF SEQ ID NOS: 989

**SOFTHARE: FRALESQ for Windows Version 4.0
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                                                                                                                                                                                                                                   Length 1614;
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Pred. No. 0.0059;
0; Mismatches 132; Indels '0;
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                                                                                                                                                                                                                                   Score 44.8; DB 18;
Pred. No. 0.0036;
0; Mismatches 72;
                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT4530_7942C.1
US-10-437-963-79739
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                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.0%;
Matches 88; Conservative
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Best Local Similarity 48.4%;
Matches 124; Conservative
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ORGANISM: Oryza sativa
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LENGTH: 3453
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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Collean M.
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Collean M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions Isolated from Plant Cells
FILE REFERENCE: 11000.10203
CURRENT APPLICATION NUMBER: U0/10/464
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR PLING DATE: 2000-11-01
PRIOR PLING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR PELING DATE: 1999-01-12
PRIOR PELING DATE: 1999-01-12
PRIOR PELING DATE: 1999-11-01
PRIOR PELING DATE: 1999-11-01
PRIOR PELING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: PastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
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4.6%; Score 44.8; DB 19;
Best Local Similarity 48.4%; Pred. No. 0.0059;
Matches 124; Conservative 0; Mismatches 132;
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Publication No. US20040123343A1
GENERAL INFORMATION:
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o. US20050050583A1
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
243 TCGGCGGCCCTTCCC 258
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; ORGANISM: Eucalyptus grandis
US-10-864-252-861
                                                                                                                                                                                                                                                Sequence 861, Applica
Publication No. US200
GENERAL INFORMATION:
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US-10-437-963-47358
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123 ACCACGACGACCTCCACGCGTTGAGGGGCCTCGCTGAGAACCTAAGCGCGCAAAGGAGCCG 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 TCCGCCTCCGCGCCCCATGGTCCGGCGCCTCATGCTGCAGCTGTGGGATGCG 242
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38 421(53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 2589
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                                                                                                                                                                                                                                                                                                                                                       Ouery Match 4.6%; Score 44.6; DB 18; Length 2589; Best Local Similarity 51.0%; Pred. No. 0.0057; Matches 132; Conservative 0; Mismatches 124; Indels 3;
                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_50134C.1
US-10-437-963-47358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: May 11, 2005, 04:32:56 Job time: 773 secs
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CR382398 Plassmodiu ACLO7560 Rattus no ACL28061 Rattus no ACL28061 Rattus no ACL24408 Mus muscu ACL341059598 Mus muscu ACC090126 Mus muscu CR222870 Desulfota ACC19509 Rattus no ACL19495 Rattus no ACL19495 Rattus no ACL19495 Rattus no ACL19495 Rattus no ACL13232 Rattus no ACL13232 Rattus no ACL13232 Rattus no ACL13495 Rattus no ACL13696 Mus muscu ACL13606 Mus muscu ACL2470 Mus muscu ACL2470 Mus muscu ACL2470 Mus muscu ACL151578 Mus muscu ACL151578 Mus muscu ACL151578 Mus muscu

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Bukaryochyta; Embryophyta; Tracheophyta; Eukaryochyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Poeae; Lolium.

CE 1 (bases 1 to 357)

RS Jarman, C.D., Sidebottom, C.M., Twigg, S. and Worral, D.
Freezed foods

AL (Dilum perenne (perennial ryegrass)

PR 2002504316-A/1

PD 12-FEB-2002

PR 23-DEC-1998 UP 2000528689

PR 22-JAN-1998 GB 9801408.7

PI CARL DUDIER JARWAN, CHRISTOPHER MICHAEL SIDEBOTTOM, SARAH TWIGG, PI CARL DUDIER JARWAN, CHRISTOPHER MICHAEL SIDEBOTTOM, SARAH TWIGG, PI DAWN WORRALL

PC C12N15/09, A0115/00, A23G9/02, A23L3/375, CO7K14/415, C12N15/00 CC

Freezed foods

Location/Qualifiers

FT source Lossanism='Lolium perenne (perennial FT / Organism='Lolium perenne (perennial FT
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/organism="Lolium perenne"
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/db xref="taxon:4522"
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E02599
HSSIGMG4
AC103606
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AC133239
AC095765
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BD139942.1 GI:23234887
JP 2002504316-A/1.
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Lolium perenne
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VERSION
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ORIGIN
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AK103166 C
AK103276 C
AK122127 F
AK372178 I
AK972178 I
AC041677 S
AC126139 F
AC126139 F
AC098103 F
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AC09818 A
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AJ277399
AK121984
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CR382398
                                                                            May 10, 2005, 23:56:18 ; Search time 4632 Seconds
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                         4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
                                                       nucleic search, using sw model
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AK121984
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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No.
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PAT 18-SEP-2002

linear

DNA

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0; Gaps

Length 357; Indels

27.0%; Score 264.2; DB 6; 83.8%; Pred. No. 2.4e-60; tive 0; Mismatches 58;

Query Match Best Local Similarity 83.8% Matches 299; Conservative

8

Rattus no Rattus no Zebrafish Rattus no Nostoc sp

231341 243639 342650

9979

290724

482 GATGAAGAACCAAATACAATATCAGGGACCAACAATAGTGTTGGATCAGGGAGCAACAAT 541

838

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Sidebottom, C.M.
Thesis (1999) University of York
2 (bases 1 to 357)
Sidebottom, C.M.
Direct Submission
Submitted (11-APR-2000) Sidebottom C.M., Plant Science, Unilever Research, Colworth House, Sharnbrook, Bedfordshire, MK44 1LQ, UNITED KINSDOM
Cds represents presumed mature peptide generated by cleavage before the first amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="ice_recrystallisation inhibition protein"
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Poeae, Lolium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GGGACAAACCATATCGTTACAGACAACAACAATAACGTATCCGGGAACGATAATGTA 240
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                                        GTTCTTGCTGGGGAATGACAACACCGTCATATCTGGGGACAACAATAGTGTGTCTGGGAGC
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    .354
/product="ice recrystallisation inhibition protein"
/note="ORF1"

               GTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACAGATGGTTAA
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                                                                                                                                                                                                                                                                                                     ice recrystallisation inhibition protein.
Lolium perenne
Lolium perenne
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/function="freezing tolerance"
/note="ORF1"</pre>
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/mol_type="mRNA"
/db_xref="taxon:4522"
                                                                                                                                                                                   LPE277399 357 bp
Lolium perenne partial mRNA for
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Matches 299; Conserv
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                   RESULT 3
LPE277399
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JOURNAL
REFERENCE
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Frozen food product
Frozen food product
Patent: WO 9937782-A 2 29-JUL-1999;
TWIGG SARAH (GB); UNILEVER PLC (GB); WORRALL DAWN (GB); JARWAN CARL
DUDLEY (GB); SIDEBOTYON CHRISTOPHER MICHAEL (GB); UNILEVER NV (NL)
Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Poeae; Lolium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACAGATGGTTAA 838
                                                                                                               61 GTTCTTGCTGGGAATGACAACACCGTCATATCTGGGGACAACAATAGTGTGTCTGGGAGC
                                                                                                                                                                                                          121 AACAACACTGTCGTAAGTGGGAATGACAATACCGTAACCGGCAGCAACCATGTCGTATCA
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GTTGTTTCCGGGAATGACAACACGGTCGTATCTGGGAATAACAACCATGTGTCTGGGAGC
                                                                                                                                                                           AACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTATCA
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Pred. No. 2.4e-60;
0; Mismatches 58
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    .357
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/mol_type="unassigned DNA"
/db_xref="taxon:452"

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Sequence 2 from Patent W09937782.
AX019971.1 GI:10043803
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Best Local Similarity 83.8%;
Matches 299; Conservative
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ACCESSION VERSION KEYWORDS

ORGANISM

REFERENCE AUTHORS

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The:

URL: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
FalS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M.,
Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M.,
Nau,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M.,
Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Harao,A., Hashizume,W., Haysshida,K., Hayatsu,N., Hiramoto,K.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kouda,M.,
Kyasi,X., Yasioh,H., Sasaki,D., Sato,K., Shibata,K.,
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Takaki-Akahira,S., Tagawa,A., Takahashi,R.,
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Takaki-Akahira,S., Tagawa,A., Takahashi,R.,
Tagami,A., and Hayashizaki,Y.
Takaki-Akahira,S., Tagawa,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
Tagami,A., Tagami,M., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
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305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 GCAACGTCGTGGTCGTGCCACCACGACGTCCACGCGTTGAGGGGCCTCGCTGAGAAC 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
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/db.rizivar="159947"
/clone="J033108010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.1%; Score 79.4; DB 8; Length 3392; Best Local Similarity 63.1%; Pred. No. 4.4e-10; Matches 157; Conservative 0; Mismatches 86; Indels 6
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AP004342.5 GI:50510014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length CDNA Project Team:, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y.; Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.; Murakami,K., Ikeda,R., Sugiyama,A., Mazuno,K., Yokomizo,S., Niikura,J., Narikawa,R., Sugiyama,A., Mazuno,K., Yokomizo,S., Niikura,J., Kawami,J., Kawamata,M., Yoshimura,A., Miura,J., Kawai,J., Kawai,J., Adachi,J., Alazawa,K., RIKEN:, Kawai,J., Carninci,P., Adachi,J., Alazawa,K., RIKEN:, Kawai,J., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Saito,R., Shiraki,T., Soshino,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Hayamida, K., Hayashizaki, Y., Hayaeteu, M., Hisamoto, K., Hiraoka, T., Hayashizaki, Y., Hayateu, M., Hisamoto, K., Hiraoka, T., Horta, I., Ilda, J., Ikada, R., Ikada, R., Ilmanra, K., Inchi, J., Inda, J., Ikada, R., Imamura, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa Hirozan, Y., Koihimoto, N., Kobayashi, M., Kodya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, Y., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Matsuyama, T., Madama, Y., Numasaki, K., Muraka, R., Numasaki, K., Matsuyama, T., Nakahama, Y., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Ooka, H., Ooka, H., Otaco, M., Ohtsuki, K., Otaka, M., Ooka, H., Osato, M., Ohtsuki, K., Sakai, C., Sakai, K., Shinasaki, R., Shishiki, T., Sagabe, Y., Sugami-Takeda, Y., Tagawa, A., Shiraki, T., Tsuaka, T., Toman, A., Shishiki, T., Sagabe, Y., Sugami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yaeunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A., Yamamoto, M., Yaeunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A., Yamamoto, M., Yaeunishi, A., Yazaki, J., Yocollection, mapping, and annotation of 28K full-length cDNA clones
                                                                                                                                                                                                                                                                             AKLZ1984 3392 bp mRNA linear PLN 29-OCT-2003
Oryza sativa (japonica cultivar-group) cDNA clone:J033108010, full
insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AK121984.1 GI:37991607
PLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba; Ibaraki
                                   japonica rice
Science 301 (5631), 376-379 (2003)
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Unpublished
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REFERENCE AUTHORS

MEDLINE PUBMED JOURNAL

TITLE

REFERENCE AUTHORS TITLE JOURNAL

JOURNAL

TITLE

7

6; Сарв

220

280

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GAEGRAAREKESERREGGGGGPREIRPIDPGGGKIDFCGGI"
complement (1507...1932)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trānslation="mrrahaQPHGSRWNARTGGTDRGRPDP1SAELVPTWRLRGAYVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-coding transcript probably inactive due to including stop codon(s) in CDS" complement(5942..6631) //gene="Po585H11.1018): AUJ01213(E2609), C72987(E2609) contains full-length cDNA(s): AK106062"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="supported by full-length cDNA(s): AK109288" 5872. .6872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="supported by full-length cDNA(s): AK106062"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-related/dirigent protein-related"

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                                                                                                                                                                                                                       /note="start and end point are not identified"
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complement(join(8221. .8529,8623. .8754))
/gene="P0585H11.105"
/note="predicted by GeneMark.hmm etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="POSSH11.106"
/note="start and end point are not identified"
complement(14091. 14753)
/gene="POSSH11.106"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="P0585H11.103"
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/genea="P0585H11.105"
/gene="P0585H11.105"
/gene="P0585H11.105"
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                                                                                                                                                                                                                                                                                                                        'note="predicted by GlimmerM etc."
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/gene="P0585H11.104"
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/gene="P0585H11.104"
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/gene="P0585H11.103"
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                                                                                                                                                                                                                                                                                                                                                                                                                       Augustical Science, Rice Genome Research Program, Kannondai 2-12, Taukuba, Ibaraki 305-8602, Japan 3-12, Taukuba, Japan 3-12, 
                          Oryza sativa (japonica cultivar-group)
Wakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-NOV-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                   Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
clone:P0585H11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Oryza sativa (japonica cultivar-group)"
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/note="retart and end point are not identified"
complement(join(298. 591,655. .792))
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                                                                                                                                                                                                                                                                                                                                            Sasaki, T., Matsumoto, T. and Yamamoto, K. Direct Submission
      (japonica cultivar-group)
                                                                                                                                                                                                                                                                                 Published Only in Database (2001) 2 (bases 1 to 149371)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (298. .792)
/gene="P0585H11.101"
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SOURCE
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Eukaryota, Allegatum Jul.,
Eukaryota, Altocolata, Apicomplexa, Haemosporida, Plasmodium.

Eukaryota, Alvocolata, Apicomplexa, Haemosporida, Plasmodium.

(E 1 (bases 1 to 349418)

RS Hall,N., Pain,A., Berriman,M., Churcher,C., Harris,B., Harris,D.,
Mungall,K., Bowman,S., Atkin,R., Baker,S., Barron,A., Brooks,K.,
Buckee,C.O., Burrows,C., Cherevach,I., Chillingworth,C.,
Chillingworth,T., Christodoulou,Z., Clark,L., Clark,R., Corton,C.,
Cronin,A., Davis,R., Dear,P., Dearden,R., Doggett,J.,
Feltwell,T., Goble,A., Goodhead,I., Monsey,T., Holroyd,S.,
Hance,Z., Harper,D., Hauser,H., Hornsby,T., Holroyd,S.,
Hance,Z., Harper,D., Hauser,H., Hornsby,T., Holroyd,S.,
Kerhornou,A., Knights,A., Konfortov,B., Kyes,S., Larke,N.,
Iawson,D., Lennard,N., Line,A., Maddison,M., McLean,J., Mooney,P.,
Rabbinowitsch,E., Rajandream,M., Rutherford,K.M.,
Sanders,M., Simmonds,M., Seeger,K., Sharp,S., Smith,R., Squares,S., Stevens,K., Taylor,K., Tivey,A., Unwin,L.,
Whitehead,S., Woodward,J., Sulston,J.B., Craig,A., Newbold,C. and
Barrell,B.G.

L Nature 419 (6906), 527-531 (2002)
349418 bp DNA linear INV 30-MAR-2004 Plasmodium falciparum chromosome 6, complete sequence; segment 1/5. CR382398 AL644505 HTG.
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Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K.,
Berriman, M., Pain, A., Hall, N., Atkin, R., Chillingworth, C.,
Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M. and
Barrell, B.G.
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Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K.,
Berriman, M., Pain, A., Hall, N., Atkin, R., Chillingworth, C.,
Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M. and
Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-MAR-2004) P.falciparum Genome Sequencing Consortium, The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A, UK
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (20-SEP-2002) P.falciparum Genome Sequencing Consortium,
The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA, UK
4 (Dases 1 to 349418)
Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K.,
Berry, A.B., Berriman, M., RA Pain, A., Hall, N., Atkin, R.,
Chillingworth, C., Doggett, J., Ormond, D., Sanders, M., Hayes, R.,
Hall, S., Quail, M. and Barrell, B.G.
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/isolate="3D7"
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                                                                                                                                                                                      3D7
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                                                                                                                                                                                    Plasmodium falciparum
Plasmodium falciparum
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                                                                          DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānblation="mswgClllllllmm1vsasssatm1v1spsnsssaaaagggrrm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 AAGCGCGCCTTGCAGCGATCATCCTCGATTGGTGAGCTTGATCACCTTCGCTAT 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 GCAACGTCGTCGTGCTGCCACCACGACGACCTCCACGCGTTGAGGGGCCTCGCTGAGAAC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="contains EST(s): AU056601(S20723),AU056602(S20723)
contains full-length cDNA(s): AK064359"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 CT---AAGCGGCAAAGGAGCCGTCCGCCTCCGCGCCGCATGGTCCGGCGCCTCATGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26336 GCTGCGGCGCCCATGCCACCCGGAAGACCTCCTCGCGCCTGCGGGCATTTGCGGGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="P0585H11.108"
complement(join(<20109. .20350,20514. .>20613))
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/note="start and end point are not identified"
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/note="predicted by FGENESH etc."
                                                                                                                                                                                                                                   note="start and end point are not identified" join(15804, .15851,16016, .16324)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="start and end point are not identified"
26261. 29293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative phytosulfokine receptor" /protein_id="BAC20742.1"
                                                                                                                                                     gene="PO585H11.107"
join(<15804. .15851,16016. .>16324)
gene="PO585H11.107"
                                                                                                                                                                                                                                                                                                                         'note="predicted by GENSCAN etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'product="hypothetical protein"
'protein id="BAC20741.1"
'db xref="G1:23617053"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (20109, .20613)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="P0585H11.109"
<26261. .>29293
/gene="P0585H11.109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="P0585H11.109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGDGEHPQPSRSLVAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon start=1
                                                                                                                                                                                                                                                                                                                                                       /codon start=1
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                                                                                                                                    15804. .16324
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KLILDHLKNNATTCKDNNSLEEDENOPKTKINPCIKRTRIPTRGASNNLVSVKHIAEL
MQRSARKQLEAGAGEINLKODATKGKYTKKNGKAVALNDICS IDVQHSNSTYRSEKPC
AGKNTGRFDIGTPWRTTUNKOMEDOYMPPRREHWCTSNLEYLETDGGPLKNSDGKF
VNHSPLGDVLLAANHEAKKIKELYTKONGLNDLKOKETYCRAKYSFADLGDIIRGKD
MDDNETGMKHAKKHLKDVFDNIRKSLKOKGNQKYNYDDKKLPPYKELREDWWEANRHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGAGESPARSDADSRGPATVGAGEVEEDGEDVDSEEEEDEVEERPAGEVCENVDTLL
DISNGGROUNDROOVQPYFGMOCKLSTPFOKERGSCHPPRAIKLCVSGLTOTNN
DISNGGROUNDROOVQPYFGMOCKLSTPFOKERGSCHPPRAIKLCVSGLTOTNN
DIFFGTDISTHIFITTGALETYPAMLRYKKINTBADKEHKGGKTPDFFRRQMFYFGDYB
DIFFGTDISTHINHIPEVSKVITTLLEKENGTKSEDKQKFNNVLLEDWWKEHGPEIWEG
KRALALINGLTDDEKKOBITKYKXSYDEDBOSSLEEFPAGTSQFTRWATBWGEBDFC
KROKEQVOFTLOKACKFFCUINAEDTKTKCRECKVYEQFIKQWFCOYEQGSKFFTTD
KVQPEYAVDADVKKSTHAYQYLSKKLKKICQNGTTTDKCDYKCMENASRQPGTSSACSQ
SQQQNKSSTENNYPBARPOCPPKEIANCKNOFFPEPEKXCOYKCMENASRQPGTSSACSQ
SQQQNKSSTENNYPBARPOCPPKEIANDAIGTTTINEKEWYKVPPPNSSCDNKSSNRFNS
EKQWLCNNINLKKKNITLPFPNDAIGTTTINEKEWYKVPPPNSSCDNKSSNRFNS
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KKLASDDQKXYKDLVNHYDLESDWMDANRRDIWAMTCAAPENAYI YKTTENSETKIR
SYDMYYYCGHKDDPPDNDIP IPQKLRMYTEWSEYFCKELNRKLEQMKTNCDSCKLNDSN
CRDSNOGNNCRKCQONCOEYTKLVNQCKKQFILQDNOYKEIYKKISNNSDGKAYVGTH
VVEFLKKVBKNKCSDLNSADRYLYKGSNCKNLIFTENDNEHRTRTYAFTEKJIEYNK
CYCEITNHPLDKCPPPQNIIICNNJYTNASYRYTIULKEWNNNLVPRISSDNYGYL
VPPRRKHICLANITANYLLNSYKKNYTIULKEWNNNLVPRISSDNYGYL
VPPRRKHICLANITANYLLNSYKKNAYINAAYNBAYFLWTYNNGSTTAFFAL
KYSFADYGDIIKGTDIMESSLSDKIGNIFTNYTNAANBAYFLWTYNNGSTTAFFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCPACVVECDGGKCEEKKNSDGTCIEAQIYTVVRDETPTPIKVLFSGDHQKDITKKLŠ
SFCKNPESENNRDYQTWQCYYKSSDYNNCEMKGSLYKVEGDPNIIVSHECFHLWVQSL
LIDTIKWETKLKKCINNTNVTNCYNKCNKNCECFENWVEQKKKEWENVNDVYKDQKQS
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KKTVDSCTROTPOLGODKQCKQYTBFITKWOPQWETWSYKYOTLYTEBAERDATSGSV
KKRTOLSKEDORVUDPLOLKQLLRNSARATRVIRAGSSATGGTTAMTPNTPYSTAG
YIHHELGKTVGCNVQTKFCKHKIGSKASGTENKEYAFREKPYDHDDACACRPPKETGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tränslation="MAPQRAEDSNKSAKEVLDEFGQQVYKEKVEKDAKIYKGELEGNL
ASSSILGETASTDKPCTFEYNKLLGARGKRHPCGNRQTVRFSDEYGGQCTFNRIKDSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HINNDVGACAPFRRLHLCDYNLEKMGSTK1KDKNVLLAEVCMAAKYEGOSILKQYEEH
KNNYPHTN1CTVLARSFAD1GD1VRGKDLFLGHQQRKRKLEENLKQMFEN1KKNNDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKISIEQVREYWWNANRDQVWEAITCHAAHSDEYFRKSTDGVTLYFDGRCGRELSSVP
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YYKSFYKKFAKSDYKKVHDFLTLLINGRYCKEGVDGKDAI DFNKTDDKDAFDRSEYCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TANDKFVIDADTCKLPTEDEIPQFHRWLIEWAKQACKEYRIRKSAFEQFCHCSTAGGL
SGLDLLKNHSCNYELTQYIGWNTWYKQYMDGFDIKFQKVKNASTNSSISENSAQEYIK
GKIEGNECDFNDMENIYEKITNRKNKDFQEILGILCFNKKIDKDKSKEILDETSSKPK
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LYSGEEYSYNVMMVNSMDI PINRDNNVYSGI DLINDTLSGNKHIDI YDEVLKRKENE
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complement(join(15065. .16126,16357. .16410))
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="erythrocyte membrane protein 1 (PfEMP1)"
/protein_id="CAG25173.1"
/db_ref="GI:4638239"
'codon_start=1
'product="erythrocyte membrane protein 1 (PfEMP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus tag="PFF0015c"
complement(join(15065. .16126,16357. .16410))
/gene="RIF"
                                                                                                db_xref="PSEUDO:CAG25172.1"
|oin|(3503. .10936,11630. .12835)
|gene="VAR"
                                                                                                                                                                                                                                                          уолп(3503. .10936,11630. .12835)
gene="VAR"
                                                                                                                                                                                                                                        locus tag="PFF0010w" |
                                                                                                                                                                                                                                                                                                                                                                            Tocus tag="PFF0010w"
note="MAL6P1.316"
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                                                                                                                                                                                AINWWKTTEIAÄATKÄAIAAGKAAGKIAGEAAGKKAVIEALKYFGVDDFFPEIFKSIL
KORSYTDVTKEGALIAEKHVLNCANSARGGSVNDSTCNAFEIKLGLFEAETGKPNGPP
AYQAIPQKINELAEERATQAABAAKKASESATAAFETAEKEAIEASMQLYTTIAYSI
LAILIIVLINVIIVLIRYRRKKKKKKLOYIKLLEE
COMDLEMENT (join (18586. 19821,19980. .22721))
                                                                                                           YAPATYDDDPQMKEVMQQFEDRTSQRFHEYDERMKTTRQKCKDKCDKE1QK1ILKDKL
EKELMDKFATLQTD1QNDA1PTCVCEKSLEDKMEKGCLRCGGVLGGG1APTFGL1GSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ONRFDENAEAYCNSDKIRGNENNSNAGACAPFRRONLCDKNLEYLINENTKTTHDLLG
NVIVTAKYEGDYIVNNHPNRGSSEVCIALARSFADIGDIVRGKDMFKSNDNVENGLRE
VFKKIYEGFLDKGAREHYKEVKNGNYIKLREDWWTANRDQVWKAMTCVAPENAYFRKT
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KDCEMSRRCNNDTEGEKCKKCKEQCQIFKELVSKWKNEFDKQSMKYKELYIKASTNIT
KQNSSSPERGYRRNHRRRGYDDDTNVQLFLKKVIENNECKVESLGKYLDKTSHCGNYN
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FPKNDL I EWNNSGVKNKENDNNGVL VP PRRRNLCI NL FSKKOYKAKDENDFKEDLLNA
AFSQCKLLGKKY SNYSNEAY FAMKFSYADY SDI VKGTDMANDLKKLNKELNTLLKETE
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KGLSEKYIKIKKSKNSGVNIPSEECAASYVTKHCNGCICNLRDMEDIHKNINNQNELM
KGMINIKRDDVYRTOLQNISNSMEINPKSYTRAVOTTKDIVSYGLAGTMGVAAIGL
QAGDFLGKKIQDLYNEFWYEKLENSSKNLNYTSDPNIMYPAGIGVALTLGLLLFK
MRRKAKROVDMIRLLQMSQNEYGIPTTKSPNKYVPVGSQRYKKKTYLYLVYGGDYDEEKY
MFRAKROVDMIRLLQMSQNEYGIPTTKSPNKYVPVGSQRYKKKTYLYLVYGGDYDEEKY
MFMSDTTDITSSESEYEEMDINDIYVPGSPKYKTLIEVVLEPSKRDTQNDIPSDNTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="G1:46362241"
/translation="MGSDYSSPGGNKSVNITESEKSARNVLEKIGRHIKDEINKNSNH
TNKLKGTLSNAQFHDGLHKAAGWGVRYGPANSCDLEHRFYTNINNGYLPARNPCHNRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YKLTDEEWNQLKDDFISQYLPNTEPNNYRSGNSPTNTNNTTTSHDNMGEKPFIMSIH
DRNLYTGEEISYNINMSTNTNNDIPKYVSNNVYSGIDLINDTLSGNKHIDIYDEVLKR
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                                                                                translation="MKIHYINILLFELPLNILIYNQRNHNSTTPHHPPNTRLLCECEI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLKEKWENDNDGGNVPSDNHVLNTDVSIEIDMDNPKPINQFSNMDINVDTPTMDNMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="erythrocyte membrane protein 1 (PfEMP1)-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   579 ATAACAACCATGTGTCTGGGAGCAACACACTGTTGTAACTGGAAGTGACAATACTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273374 ATAACAACAATATGGTGGATGATAACAACAATATGGTGGATGATAGCAACAATATGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273314 ATGATAACAACAATATGGTGGATGATAACAACAATATGGTGGATGATAACAACAATATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATACTGTATCAGGGGAGCACAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /locus tag="PFF0020c"
/note="Does not produce Pfam hit to PFEMP domain
(pfam:PF03011), found in Pfempl protein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="PFF0020c"
complement(join(18586. .19821,19980. .22721))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 349418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus tag="PFF0025w"
join(26557. .26610,26766. .27830)
/locus tag="PFF0025w"
/note="MAL6P1.313"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(26557. .26610,26766. .27830)
/gene="RIF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.7e-09;
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55.8%; Pred. No. 8.7e-09
/protein_id="CAG25174.1"
/db_xref="GI:46362240"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein id="CAG25175.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                possible pseudogene
MAL6P1.314"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="VAR-like"
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Matches 145; Conserv
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UNAS Rice Full-Length CDNA Poojekt Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M. Fals Genome Sequencing & Analysis Group: Otcomo, Y., Iida, Y., Rodama, T., Kurosaki, T., Kubibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kuumegi, T., Lu, M., Masuda, H., Muta, J., Kodama, T., Kurosaki, T., Tsunoda, Y., Uoka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Uoka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Uoka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Uoka, M., Kie, O., Yokomizo, S., Yoshimura, A., Matsubara, K. Hakani, Y. Haradawi, Y., Arakawa, T., Carninci, P., Pukuda, S., Hanagaki, T., Arimara, T., Arakawa, T., Harada, T., Harada, T., Harada, T., Harada, T., Harada, T., Harada, T., Kojama, Y., Katoh, H., Kawai, J., Kawai, J., Kanoo, H., Kawai, J., Kanoo, H., Kawai, J., Kanoo, H., Kawai, J., Kanoo, H., Kawai, J., Sakai, C., Sakai, K., Sakazume, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Cata, Y., Zatoh, H., Sakai, C., Sakai, K., Sakazume, M., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Taqawa, A., Takahashi, F., Takakh-Akhira, S., Tagama, T., Wasui, K., Yasunishi, A. and Hayashizaki, Y., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y., Towaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y., Towaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y., Towaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y., Towa, T., Yoya, T., Waki, K., Yasunishi, A.
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Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 TTGGAGGGATCATCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTATTTGGATCTCT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK103166.1 GI:32988375
F1LCORM, CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Guyza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 CGGGTAATTCATTGGTTGGGGAGGTACCAAAAGTTTGCAGATACGGCTCAAGAGAGCCTCA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group) cDNA clone:J033121E13, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3, Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/culfivar="Nipponbare"
/db xref= txxon: 39947"
/clone="002-108-B08"
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                                                                                                                                                    : http://cdna01.dna.affrc.go.jp/cDNA/
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Pred. No. 7.1e-09;
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7.6%; Score 74.8; Diabet Local Similarity 68.4%; Pred. No. 7.1e
Matches 119; Conservative 0; Mismatches
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KEYWORDS
SOURCE
ORGANISM
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AK103166
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                                                   COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Locati, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M., Hizahda, K., Hayashizaki, Y., Hayafteu, M., Hizamcto, K., Hiraoka, T., Hayashizaki, Y., Hayafteu, M., Hizamcto, K., Hiraoka, T., Hori, F., Hotta, I., Idda, J., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koda, M., Koda, M., Kodama, T., Kojima, K., Mirosaki, T., Muneugi, T., Li, C., Lu, M., Masuda, H., Matsubara, C., Kurosaki, T., Muneugi, T., Li, C., Lu, M., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namura, M., Namiki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Oosato, N., Otca, Y., Otomo, Y., Ryu, R., Satoh, H., Sakai, C., Sakai, K., Shinagawa, A., Saraki, T., Shishiki, T., Soqabe, Y., Sugano, S., Sugano, S., Sugayama, A., Takahahi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yanada, H., Yanamaoto, M., Yasunishi, A., Yasaki, J., Yokomizo, S. and Yoshima, A., Yasamahi, A., Yasawi, J., Yasawi, J., Yokomizo, S. and Yoshima, A., Lanaka, J., Yasawi, J., Yokomizo, S. and Yoshima, A., Yasawi, J., Yasawi, J
                                                                                                                                          273194 TGGTGGATGATAACAATATGGTGGATGATAACAACAATATGGTGGATAATCACAATA 273135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group) cDNA clone:002-108-B08, full inser sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLI_CDNA; oligo-capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Submitted (05-DEC-2001) Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
                                              CCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 301 (5631), 376-379 (2003)
                                                                                                                                                                                                                                                                                                                                        273134 CTATGCGTAGCGAAGATGAA 273115
                                                                                                                                                                                                                                      819 AAGTCGTAACAGATGGTTAA 838
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VERSION
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ORGANISM
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JOURNAL MEDLINE AUTHORS

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SOURCE
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Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group. Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kuroaski, T., Kodama, T., Mauda, H., Kobayashi, M., Xie, O., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusunegi, T., Oka, M., Ryu, R., Yoshimura, K., Arakawa, T., Fukuda, S., Kawai, J., Carninci, P., Adachi, J., Aizawa, K., RIKEN: Kawai, J., Knaki, Konno, H., Miyazaki, A., Otato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagaahira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         japonica rice
Science 301 (5631), 376-379 (2003)
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REFERENCE
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COMMENT

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CNSO8CBF
Human chromosome 14 DNA sequence BAC R-731F5 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1085 CAAACAATTCCTTAGTCGGCGAGATACCGAAGAGTTT---GACGCAGCTCAAGAGCCTTG 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 CGGGTAATTCATTGGTTGGGAGGTACCAAAAGTTTGCAGATACGGCTCAAGAGCCTCA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotan, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to 17623)

Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, B., Artiguenave, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, B., Artiguenave, P., Gyapay, G., Saurin, W. and Weissenbach, J.

Sequencing of the human chromosome 14

Unpublished
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Submitted (19-SEP-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                   TIGGAGGGATCATCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTATTTGGATCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                       1025 IGGTTGGCACCATCCCTGAATGGATCGGTCAACTTGATAACCTGACCTACTTGGATCTTT
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1142 TCACCGCCCGACGTTCGCCGGGTATGGCGTTCACTAACATGCCGTTGTATGTGA 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the SP6 end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464
                                                                             /organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Sep 24, 2002 this sequence version replaced gi:23306222.
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Quality coverage: 11.37x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 CCACTGACAGCCAGTCACTCGGTATGGGTTCCATTAACATGCTATTGCATGTGA
                                                                                                                                                                                                                                                                                                                             3,
                                                                                                                                                                                                                                                                         Length 2958;
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                                                                                                                                                                                                                                                                    Score 74.8; DB 8;
Pred. No. 7.5e-09;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.genoscope.cns.fr/
Contact: SegRef@genoscope.cns.fr
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                                                                                                    /mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J033121E13"
Yasunishi, A. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Center
                         Location/Qualifiers
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                                                                                                                                                                                                                                                                    7.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: GS
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                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 119; Conserv
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Overall quality chart :
Range : bases
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                                                             AL122127
AL122127.6 GI:17026193
                                                                                                                                                                                                                                                                       (bases 1 to 169802)
                                                                                                      Homo sapiens (human)
Homo sapiens
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55713
56253
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               CNS01DT2
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VERSION
KEYWORDS
SOURCE
ORGANISM
                 LOCUS
DEFINITION
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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
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   CNS01DT2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7724 CAGGAAGCATCCAGAGTGGAACAGGAAATGTCCAGCATGGAACAGGAAGCATCAAGAATG 7665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7664 Taacadgaagcarccagagriggaacaggaaargriccaggaacaggaacaggaagcarccaga 7605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600 GCAACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTAT 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGGACAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAATG 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTCTGGAAGCTTCCATACTGTATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATA 779
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                                                                                                                                                                                                                                                                                                                            dbSTS:STS21065
Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                    dbSTS:STS48887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dbsTS:STS56700
Identified using the e-PCR software (G. Schuler)"
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Identified using the e-PCR software (G. Schuler)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                780 CIGIAICCGGGAGCAACCAIAICGIAICTGGGAGCAACAAAGICGIAACA 829
                                                                                                                                                    >= 40 : 99 %.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dbSTS:STS37918
Identified using the e-PCR software (G.
                                                                                                                                                Percentage of bases with a quality value Location/Qualifiers 1. .176237
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                                                                                                                                                                                                                                                                                                                                                           57606. .57752
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                                                                                                                                                                                                                                                       clone="R-731F5"
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                                                                                                                                                                                                                                                                                                                                                                                           RHdb:RH68981
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                                                                                                      54448
79950
110 - 129
220 - 229
440 - 149
550 - 559
60 - 69
90 - 89
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RESULT 10

CNS01DT2 169802 bp DNA linear PRI 19-NOV-2001 Human chromosome 14 DNA sequence BAC R-417P24 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence. Genoscope.

Direct Submitssion
Submitted (19-NOV-2001) Genoscope - Centre National de Sequencage :
Submitted (19-NOV-2001) Genoscope - Centre National de Sequencage :
Submitted (19-NOV-2001) Genoscope - Centre National de Sequencage :
Submitted (19-NOV-2001) Genoscope :
Web : www.genoscope.cns.fr) Bukaryote, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria; Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 169802)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottier,P., Cattolico,L., Barbe,V., Pelletier,B., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Sequencing of the human chromosome 14

Unpublished The following BAC sequence is oriented from the T7 to the SP6 end. On Nov 20, 2001 this sequence version replaced gi:14715169. Identified using the e-PCR software (G. Schuler)" 39191. :39405 /note="matching EMBL:G33053 RHdb:RH67749 dbsTS:STS47676 Identified using the e-PCR software (G. Schuler)" 11439. .11536 /note="matching EMBL:G14654 Percentage of bases with a quality value >= 40 : 99 %. Location/Qualifiers Assembly program: Phrap, version 2.0 Ouality coverage: 7.56x in Q20 bases; sum-of-contigs Center: Genoscope / Centre National de Sequencage Center code: GS Web site: http://www.genoscope.cns.fr/ Contact: SeqRef@genoscope.cns.fr 11427._.11641 /note="matching EMBL:G33053 RHdb:RH67749 organism="Homo sapiens" /mol_type="genomic_DN /db_xref="taxon:9606" /chromosome="14" /clone="R-417P24" /clone_lib="RPCI-11" ----- Genome Center STS

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Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Bucke, C.O., Burrows, C., Cherevach, I., Chillingworth, T. Chistedoulou, Z., Clark, L., Clark, R., Corton, C., Cholin, A., Davies, R., Davis, P., Dear, P., Dearden, F., Doggett, J., Feltwell, T., Goble, A., Goodhead, I., Gwilliam, R., Hamlin, N., Hance, Z., Harper, D., Hauser, H., Hornsby, T., Holroyd, S., Harper, D., Hauser, H., Hornsby, T., Holroyd, S., Karbornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Lawson, D., Lennard, N., Oliver, K., Ormond, D., Price, C., Quail, M.A., Rabbinowitsch, E., Rajandream, M.A., Rutter, S., Rutherford, K.M., Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R., Squares, S., Stevens, K., Tavey, A., Unwin, L., Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and Barrell, B.G.

Nature 419 (6906), 527-531 (2002)
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YKTREDESGEEKSGTLEEDSYGTLEEDSYGTLEEDSYGTLEEGYGEETREGE
GTXEEDSEDSEEFYGTLEEDSYGTLEEDSYGTLETGEGYGSPERFYGTLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 AAGAATATCGTACCCAAGAGGAAGAATATCGTACCCAAGAGGAAGAATATCGTACCCAAG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 AGGAAGAATATCGTACCCAAGAGAAAGAATATCGGACCCAAGAGAAGAAGAATATCGTACCC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       725 GGAAGCTTCCATACTGTATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATACTGTA 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 AAGAGGAAGAATATTGGACCCGAGAGGAAGAGTATAGGACCCGAGAGGGAAGAATATAGGA 271
                                                                                                                 /note="grass-specific insert; similar to Oryza sativa sequence deposited with GenBank Accession Number X15901"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hamlin, N., Pain, A., Berriman, B., Hall, N., Bowman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Quail, M. and Barrell, B.
                                                                                                                                                                                                             polymerase beta' subunit 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          665 ACAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAATGTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                605 AACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTATCAGGG
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Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 646;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCAAGAGGAAGAATATCGTACCCAAGAGAAAGAATATAAGACCCGA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              6.5%; Score 63.8; DB 8; Ilarity 55.1%; Pred. No. 5.4e-06; Conservative 0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                /codon start=1
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db xref="taxon:158113"
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Plasmodium falciparum MAL4Pl.
AL034557 AL844503
AL034557.8 GI:23498126
                      <1. . >646
/gene="rpoC2"
                                                                                          gene="rpoC2"
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Best Local Simi
Matches 125;
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ACCESSION
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                      gene
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19413 AGAAACATCCAACATGGAACAGGAAGCATCCAGAATGGAAAAGGAAGCATCCAGCATGGA 19472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19533 GGAACAGGAAGCATGCAGAGTGGAACAGGAAATGTCCAGGATGGAACAGGAAGCATCCAG 19592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF372178 646 bp DNA linear PLN 18-JUN-2002 Leptocoryphium lanatum DNA-directed RNA polymerase beta' subunit 2 (rpoC2) gene, partial cds; chloroplast gene for chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poales; Poaceae; PACCAD
clade; Panicoldeae; Paniceae; Leptocoryphium.

1 (bases 1 to 646)
Duvall, M.R., Noll, J.D. and Minn, A.H.
Phylogenetics of Paniceae (Poaceae)
Am. J. Bot. 88 (11), 1988-1992 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCAACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  659 TCAGGGACAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19593 CATGGAACAGGAAGCATCCAGCATGGAACAGGGAGCATCCAGAGTGGAACAG 19644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              779 ACTGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACAG 830
               (G. Schuler)"
                                                                                                      dbSTS:STS21065
Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                             Schuler) "
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                                                                                                                                                                                                                                                                                                                                                                                                                                               RHdb:RH51956
dbsTS:STS23199
Identified using the e-PCR software (G. Schuler)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 103; Indels
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          dbsTS:STS51071
Identified using the e-PCR software
131895. .132128
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Direct Submission
Submitted (18-APR-2001) Biological Sciences,
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/organism="Leptocoryphium lanatum"
/organelle="plastid:chloroplast"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 67.2; DB 9;
Pred. No. 1.8e-06;
                                                                                                                                                      39281. .39447
/note="matching EMBL:X99549
                                                                                                                                                                                                                                                                                                          note="matching EMBL:X00253
                                                                                                                                                                                                                                                                                                                                                                                                                              note="matching EMBL:R05773
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                                                                                                                                                                                                           RHdb: RH71306
                                                                                                                                                                                                                                                                                                                              RHdb: RH18069
                                                                                       RHdb: RH7974
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SOURCE
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AUTHORS
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FEATURES

COMMENT

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Direct Submission
Submitted (24-FFB-1999) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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SSLTRETLWKEHAPSIWEGMICALTYKENDEKKIVKDNEVYEKFFGTTPGTTSGKYKE
KYEYNTVKLDENSDTEAKDTKATAPSDNTPTFLSHFVLRPPYFRYLEEWGETFCKERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YESARREKLENKLKEVFGKI HGGLSEBAKKKYODGDGNYYQLREDWWTANRETVWKA I
TCEVKSGNNY PRATCGDEKNPSLTSKQCRCDKDKAGKP I KGSGNVNI VPTYFDYVPQY
LRWPEBWAEDPCRLRKHKLKDA I KKCRGKNGEEKYCDLNRYDCKNTASGKHVFFEDFD
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TFYRTKYCEACPWCGAEKVEGGWKAKEENCSQTKDYDPDKTTTI EI LIGDTRKSDMVQ
KYKKFCNGNGGNGEKSATPNATSREKGKKGDQMEKWI CYYDENKEKKYGSDAINFCVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCFEKWYKQKKEKEWEAIKDHFGKQKDIIEQTGCDAGYTLAAVLKLEFLNEDTEEKS
EKGLDAEEAKEIKHLRQMLEQAGVRDLAAVGGPCTEGGVAEQNTIMDKFLDEELKEAE
OCKNCPKPKAQQEGPGGARSADSPPAGTEDHPDAEDDDDEDDDDDDDDEDEEEEEEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EWGEEFCAERGKLEQNIGKSCNGINPIQYCSDNRHPCNYACDEYKNYVETKQKEFRGQ
TTKFVRDANLENADQEYKDYKTTQGPSKQGNDYLKDKCDNKKCSCWEGNVLTDVSSKK
PFGIYAHKYSEKCNCLGAKFVPTNVPPAPPPQPPPPAIPAIPAFATTPGVNPCEIVNTLF
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NQGSICVPPRRRKLYVTPLTKWAEETTKGSKSQESGKAEGTSESSGSEASSPGGTSSQ
GEKSPQGLSTPASTSSPSNSRDDDLLKAFVESAAVETPPLWHKYKMDKQKELDEKKKQ
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KI EFNEQSET FKHTKHCDPCSSFKI DCRNGKCKSGDTKGKCDGI TTI DAKEI AKMI SS
TPDVVMRVSDNDTNTFEGDDLKVCEGKGI FKGI RKEEWKCRNECGLDVCGLKKGDNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Similar to Plasmodium falciparum variant-specific
surface protein var-2 SWALL:Q26033 (EMBL:L40609) (2664 aa)
fasta scores: E(): 7.8e-149, 43.1% id in 2872 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CKDCQYSCAPFVDWIDNQKLEPLKQRKKYTKEITSGGSCGGSGRKKRDATTTNYEEYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDGKQHRKEQKVTSYNAPFWKWVHDMLHDSVEWRERLNSCINNAKSQNCKNNEKCNKE
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YYIAHESETKNIETQDDLRDAFIRTAAAETFLSWQYYKIKNGADAKQLDNGTIPEEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKLAQIKVDCKVDSADYKCSGYGEECKIEDISNIGVFADLKCPGCGRECRKYKKWIER
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KKKTKSTIDLLRVINIPKSDYDIPTKLSPNRYIPYTSGKYRGKRYIYLEGDSGTDSGY
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NTTASGNNTTASGKNTPSDTQNDIQSDGIPSSKITDNEWNTLKDEFISQYIQSEQPKD
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                                                                                                                                                       On Oct 3, 2002 this sequence version replaced gi:5731897. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product="erythrocyte membrane protein 1 (PfEMP1)"
/protein_id="CAD49094.1"
/db_xref="G123498127"
/db_xref="G481220"
/db_xref="GA04:081220"
/db_xref="GA04:081220"
                                                                                                                                                                                                                                                                                                                                                          organism="Plasmodium falciparum 3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="VAR" .41725,42757. .44124)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(35153. .41725,42757. .44124)
/gene="VAR"
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                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/isolate="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 xref="taxon:36329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="MAL4P1"
10384. .32958
/note="rep20 Repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="synonym:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome="4'
                                                                                                                                                                                                                                                                                                                  .347582
                                                                                                                          CB10 1SA, UK
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                                                                                                                                                                                                                                                                                                                                  source
    TITLE
JOURNAL
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NULYTAKYEGESI VAKHPHKENSEVCTALARS FADIODI VRCKDMFKRNEEDAVQKGL
RAVFKKI NDNLKEKEI SDYDNDPNYYLREDWWTANRDQWRAITCY I PYYVNY FKKT
BODDI VPFTNIOCKCGHYEGAP PYNLDVYPQFLAWFDSMAEFEK FRI RINHELKK KDACRA
DKERLYCSQNGYDCTKRI EKGES GSRENKCTGGSNKCVDY DFWLEKQQNEFKI QKDK
DKEI LYTVOKTPI SWOSSCRENKTGGSNKCVDY DFWLEKQONEFKI QKDK
DKEI ETYVNKTPI SWOSSNYTKESY FKEFYEELKOY GSYKNELQLINGRY COEKIEE
EDAI DFTKTGNKHAFYRSDY CQPCPOCVVECDGKTCTQKTDDDKNCRSKI I QKI LESE
TPEI EI EVI YSDDKQGY I TEKLAD FCRGPNNYNDENLQKMKYNNSESTNKCENI SWLY
QDPKEYNLALS SOECFHSWAKNLI IDTIRWEHQLKNCINNTNYTDCTSKCI IKNCECY E
NI ERKKDGWEKLKED SKOLKNOYDSTSHNYTNKLKOV FDR PLEQVMFALDQDEKGKWDQFTE
DLKKKRFGPS VESAGTANSQDA I EFLLDHLKDNALITCRDNNS I KPCTY PPNPFTPPPCGT ISSTGNYTKYTEFVNTIYSKYNGTCNLMRSSINPTACYTIETELSIKTGGAGTGDHPP LYAIROMIKGLAEEATEAAKAAEAAKNAKLTAAIKEKOTALIEAGFNSSITSINASII AILIIVLIMVIIYLILRYRRKKYMKKKLOYIKLLKE" NGKANLYSGQNAVYSGIDPTSDNRGLTSGKHDSYSGIDLINDTLSGNQHIDIYDEVLK KENELEGTHVKHTTINFREKRARDDDLHNQLELFHTWLDBHRHNMCERELLD KLKEEWENETHSGATTIONSTLATDVSIQIDMDNPKPINQFTNMDINVDTPTMDNM EDDIYYDVNHDTSTVDSNTHMDVSKVQIEMDVNTKLVKEKYPIADVWDI" /translation="MCTGSSTPSVPKDVKNESHNSARNVLENIGIEIYNEKKKVNGY TSQLRGDLSRARFHDGLRKAARLGVIPGPANSCDLDHKFYTNINNGYPPARNPCDLRN ONRPGENAEAYCNSDKIRVTGKKSAGGACAPPRRQNMCDKNLEYLDNTWTDDTDDLLG APATYDDDPQMKEVMVKFSKQTQQRFHBYDERMVEKRMQCKDKCDKEIQKIILKDKME NNNGGKLVRVKRLAEMMQRRARKQLEKRGGEINLKADASQGKYIRGGKEKKLNGQICN IDTSYSNDSRNGNNGGPCTGKNDKRPKIGTEWSYGEHEKKRTHPEVYMPPRREHMCIS NLEKLDVVSVI KNGNASHSLLGDVLLAAKYEAKNI KELYQQNNSKNGVI DQNDKETIC RAMKYSFADIGDI I RGKDMWVQNTDATKLQAYLAKI FDKI KDNHKDI KGKLQYNGDTD QSRLYGELLEKCQSCKGKQKCTEGDVDCGKCKAACDKYKDEINKWREQWTKIKGKYKT LYKKATKPGVTTSNNPKDEKDVVDFLKQLLPRKSKNTPGVTAMTPNTLYSSAAGYIHQ translation="MKIHYINILLFELPLNILIYNQRNHKSTNLHTQNNRSLCECELY" KELMDKFATLQTDIQSDAIPTCVCEKSLADKVEKGCLRCGYGLGTVAPTVGLIGSVAV HVWKPKALEAAI AKA I AEGTADI AAAAEAAGKARGMEFV I KALKHFGVENFFPGI CDT /note="Similar to Plasmodium falciparum variant-specific surface protein var-3 SWALL:Q26032 (EMBL:L40609) (3006 aa) fasta scores: E(): 6.2e-103, 43.31% id in 3551 aa" HKLLREDWWEANRHQVWRAMKCAI ENDKDMKCNGI PI EDY I PQRLRWMTEWAEWY CKE ELGKTVGCNTQKEPCDNKKGKYAFKHPPKEYEEACI CDTRQKAQKP I EKKNDCNG I KT LLDRSNGGTGGI DGCNPKI GNYPSWNCERNESKAENKGACVPPRREKFCVSLLAKEGI FKNKGEDIRETFVKSAALETYFAWKRYNDDNKKAEEELKSGTIPENFKRQMYYTFADY RDI FFGTDITSHDHILDVSKNAKNKLKEKNGEQKSVIIIDDEKLLADWWKEHGHEIWE REREKKEEVVEKKCKKDHEGCNKPNTKGNHGCVSACKDYEEYISTKKKQYNTQKEFD IDKNKGNEEYENYKDKEAHDYLKDKCFPGTCDYMEKVKNNSEYMDKPNKTYTNSDLEK GMLCALTHEIDEEEKNKIKSTYSYDQLKKTTNGTTPLEKFAERPQFLRWFTEWSDEFC Similar to Plasmodium falciparum rifin pfb0030C SWALL:096112 (EMBL:AE001367) (370 aa) fasta scores:-E(): 3.4e-65, 53.6% id in 375 aa" for /product="erythrocyte membrane protein 1 (PfEMP1)"
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/db_xref="G0A:081218"
/db_xref="UniProt/TrEMBL:081218" ď /note="1 probable transmembrane helix predicted TWHMM2.0 at aa 328-350 could be alternate exon II /note="synonym: PFD0020c" complement(join(52002. .53297,54200. .63307)) complement (join (48479. .49537,49768. .49821)) complement (join (48479. .49537,49768. .49821)) complement (join (52002. .53297,54200. .63307)) protein_id="CAD49095.1" |db_xref="G1:23498128" |db_xref="Uniprot/TrEMBL:Q81219" PFD0005w" 'note="synonym: PFD0015c" exon II, gene 45458. .46601 /gene="PFD0010w" 45458. .46601 'product="RIFIN" /gene="PFD0010w" codon_start=1 start=1 upstream VAR gene="VAR" gene="VAR" note="VAR 'gene≃"RIF codon

gene

SOS

672

61

732 121 792

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233583 GTTATTACAATATTGTTCATGGTTATTATATTTGTTCAGGGTTATTACAATATTGTTC 233642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233643 AGGGTTATTACAATATTGTTCAGGGTTATTACAATATTGTTCAGGGTTATTACAATATTG 233702
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                                                                      MLQTWKEHYEKOKI KYENDKDSYTNDPDTKGSPQAYOYLAKKLEKI CPSGANTSANCEY
KCMKYPSSQNNNNMPASLDDTPSDYKDTCECTKSQASSRNFSVRSEDGEDGPPPPRAP
ROSLARSADNESPRAPEGGPOPPSGTPDAGGARAETGEPSOPPKDFAGGGGVARLI
QPIARACHONEEEDEDDDESSCSEEGGEGGEGDVDDSDSSEDENDEEDEDDSHAVDGGH
QBEEPPDETEVVEEDDEDDDDESSCSSEEGGFGCOVDDSDSSEDENDEEDEDSHAVDGGH
PSGDSTTTSSVNGDRSQRHRRAAGEATGKSDASCSI CVPPRRRLYVGKLTQWASQRY
GGGTSQ1 VGKTASQPNSHPTLASPSNRDDGLADAF (QSAAVETFEHWDRYKKLNTK
KPDATLGGLPOL PLAMAAI NGYVPSGDDNNPQKKLEGGEI PEFFKGMFYTLGDYRDI
LFGKNDI VI GNTGSGASDKEMKAKEEKI KETI DKVFPNSVSTPPPTPATREDSTRU
WWEANGEHI WKGMI YALTYKDNGEKKI VKDNEVYKKLWDEANKRPKETTKY OYKNVKLE
                       KNPGDLSRKDWWNENGPYIWKGMLCSLEKAWGKDTIKNKSNYNTHNVREDDNRNGPDL
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DLQNQLESGIIPDDFKRQMFYTFGDYRDFLFGTDISKGHGIGSELAKKIDSLFKNIGG
                                                                                                                                                                                                                                                                                                                                                                   ENSGAKPTQPPSPSGDNTPTTLTNFISRPPYFRYLEEMGETFCRERKKRLEEVRKECR
                                                                                                                                                                                                                                                                                                                                                                                                GEYPGEKYCGGDGHDCTENGELKHTNMPADLDCRDCHKQCRKYRKWIDIKFEEYEKQK
DKYQGELDKLNGNSNGNNNCCKEIKKHTSASEFLKELKHCKDGQNSEDDTDKSEEDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNKI DFNKPLETFNPSTYCETCPSNKVNCNGSGRGTRGKDPCTPHNEKGKSWESVFNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKTD I CKLKNFNDKI DLAQYTTFKVFLEYWLQDF I EGYY I LKKRK I I EQCKENGGETC
NENSKNDCACVKGWVAQKTTEWNQ I KDHYNKKEYGNGYDMSHKVKNY FEKNENELRKW
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233523 ATTIATATIATATGAATGATTACTTGTTGAATATTATTGTTTTTATAATATTGTTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.5%; Score 63.8; DB 3; Length 347582; 50.5%; Pred. No. 1.8e-05; ive 0; Mismatches 152; Indels 0;
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Patent: WO 02068579-A 27611 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
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Sequence 27611 from Patent WO02068579.
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Matches 155;
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AUTHORS
TITLE
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/organism≃"Homo sapiens"

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L (Dases I to 2618)

I (Dases I to 2618)

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, D., Barder, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, D., Barder, M., Barder, M., Barder, H., Bardaranaike, D., Barber, M., Barastead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bradhar, C., Burch, F., Burrell, T., Calderon, B., Cardenas, V., Carter, K., Carter, K., Carter, M., Charder, J., Chavez, D., Chen, G., Chen, G., Chen, Y., Chen, Z., Chu, J., Chaveland, C., Davall, R., Cook, C., Coyle, M., Cree, A., Disoula, L., Davila, M., L., Davila, M., Eugene, C., Evans, C.A., Polnh, H., Divya, K., Dralla, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, S., Finley, M., Flagy, N., Forbes, L., Foster, M., Gabis, A., Ganta, M., Garcia, A., Garrer, M., Guerza, M., Gabis, A., Haaland, W., Hamil, C., Hamilton, K., Harnandez, S., Finley, M., Hamil, C., Hamilton, K., Harnandez, M., Haves, A., Henderson, N., Hernandez, J., Howels, S., Hulyk, S., Khan, Z., Kopis, L., Lobow, H., Levan, C., Luck, M., Mangum, A., Mangum, B., Mapua, P., Martin, R., Martin, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 GCAGAGTGGAACAGGAAATGTCCAGCATGGAACAGGAAGCATCCAGCATGGAACAGGAAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC126139 261587 bp DNA linear HTG 10-MAY-2
Rattus norvegicus clone CH230-104014, WORKING DRAFT SEQUENCE, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 GAGTGGAACAGGAAACGTCCACCATGGAACAGGAACCATCCAGAGTGGAACAGGAAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                         TGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCA
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0
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Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                    Score 62.8; DB 6;
Pred. No. 8.7e-06;
0; Mismatches 97;
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AC126139.7 GI:30520607
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                                                                                                                                                                                                    6.4%;
ilarity 55.5%;
Conservative 0
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Matches 121;
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                                                                                                                                                                                                         Query Match
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255148: contig of 1581 bp in length
249 255248: gap of unknown length
249 256807: contig of 1559 bp in length
256907: gap of unknown length
25808 25858: contig of 1678 bp in length
2586 25868: gap of unknown length
2586 250166: contig of 1481 bp in length
257 260266: gap of unknown length
257 261267: contig of 1321 bp in length
257 261267: contig of 1321 bp in length
257 261267: contig of 1321 bp in length.
                                                                                                                                                                                                                                                                                                                                             organism="Rattus norvegicus"
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complement (246622. .247488)
/note="clone_boundary
clone_end:Spē
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .2511
/note="wgs_end_extension
clone_end:T7"
2562. .3793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="wgs_end_extension
clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-104014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         end_sequence:BH325437"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="clone_boundary
clone_end:T7
site:EcoRI
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260167
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AC119701/c
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:24819414.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig sedfold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
Reilly, B., Reilly, M., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Rives, C., Roddev, T., Rojas, A., Rose, M., Richards, S., Riggs, F., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajs, D., Steimle, M., Strong, R., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, W., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Walas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Walliams, G., Willson, R., Waczyk, R., Weick, W., Worley, K., Wight, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 261587)

Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Atlas 3.0;
Consensus quality: 245312 bases at least Q40
Consensus quality: 249138 bases at least Q30
Consensus quality: 252151 bases at least Q20
Estimated insert aize: 257796; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shotgun sequence only contigs will be indicated in the feature table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250010: contig of 250010 bp in length 250110: gap of unknown length 253467; contig of 3357 bp in length 253567; gap of unknown length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center project name: GHUJ
Center clone name: CH230-104014
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Direct Submission
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Rattus norvegicus clone CH230-462N7, WORKING DRAFT SEQUENCE.
AC119701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             632 ACTGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCATATTGTTACTGATAACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83693 T-----GIATCAGCACTGTTAACATGTATCAGCACTGTTGTAGCATGTATCAGCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    512 AACAATAGTGTTGGATCAGGGAGCAACAATGTTGTTTCCGGGAATGACACACGGTCGTA
                                                                                                                                                                                                                                     6; Gaps
Query Match 6.2%; Score 60.8; DB 2; Length 261587; Best Local Similarity 51.9%; Pred. No. 0.00011; Matches 165; Conservative 0; Mismatches 147; Indels 6;
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RE MELLUS.

RE MARTINE, Merzker, Leer, Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, J., Alsprooks, S., Amin, A., Augulano, D., Allen, C., Allen, I., Alsprooks, S., Amin, A., Augulano, D., Allen, C., Allen, I., Alsprooks, S., Amin, A., Barnetead, M., Benahmed, F., Balden, D., Bandaranaike, D., Barber M., Barnetead, M., Benahmed, F., Balden, D., Bandaranaike, D., Barber M., Barnetead, M., Benahmed, F., Cherlo, C., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:23908282.
The sequence in this assembly is a combination of BAC based reads
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Rat Genome Sequencing Consortium.
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COMMENT

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* NOTE: Estimated insert size may differ from sequence length

(see http://www.ngsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* In 172927: contig of 172927 bp in length.

* Location/Qualifiers
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                        contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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may extend beyond the ends of the clone and there may be sequence
                                                                                                                                                                                                                                                                                   580 TAACAACCATGTGTCTGGGAGCAACACACTGTTGTAACTGGAAGTGACAATACTGTAGT
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                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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6.1%; Score 59.6; DB 2;
Best Local Similarity 52.4%; Pred. No. 0.00021;
Matches 131; Conservative 0; Mismatches 119;
                                                                                                                                    Center: Baylor College of Medicine
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|mol_type="genomic DNA"
|db_xref="taxon:10116"
|clone="CH230-462N7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         end_sequence:BZ144778"
complement(167491, .168569)
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clone_end:T7"
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172320 AGCATGTATCAGCACTGGGGTAGCATGTATCAGCACTGTTGTAGCATGTATCAGCACTTT 172261
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760 CGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAA 819		172260 TGTAGCATGTATCAGCACTGTTGTAGCATGTATCAGCACTGTTGTAACATGTATCAGCAT 172201
CGTATCCG	_ =	TGTAGCAT
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⁸²⁰ AGTCGTAACA 829 | | | | | | | 172200 TGGTATAACA 172191 È

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